

human MRPQGAASPQRLRGL--LLLLLLQLPAPSSASEIPKQKQALRQREVVDLYNGMCLQGPAGVPGROGSPGANGIPGTPGIPGRDGFKGKGECLRESF  
 mouse MHPQGAAPPQLLGLFLVLLLLLLQLSAPSSASENPKVKQKALIRQREVVDLYNGMCLQGPAGVPGRDGSPGANGIPGTPGIPGRDGFKGKGECLRESF  
 rice\_fish WTPLSPRLILLCLALPLHGQE--KGRSRGYRKDPDADKF--GSCLOGPAGTPGRDGNPGANGIPGTPGIPGRDGLKGEKGEVCVSEVF  
 abra\_fish MGTKLTQLLLICFWISLPLFCVTQKAKERIPRQ-RDAEFTDKYQA-CVQGVPGVQGRDGNPGINGIPGTPGIPGRDGLKGEKGEVCVSEVF  
 chicken RPREVLEAYNGVCLQGPSVPGRDGNPGTNGIPGTPGIPGRDGNPG.GVPGRDGNPG.NGIPGTPGIPGRDG.KGEKGECLRESF  
 nsensus .....ll.....p.....k.....r.#v...yng.CLQGP.GvpGRDGNPG.NGIPGTPGIPGRDG.KGEKGECLRESF

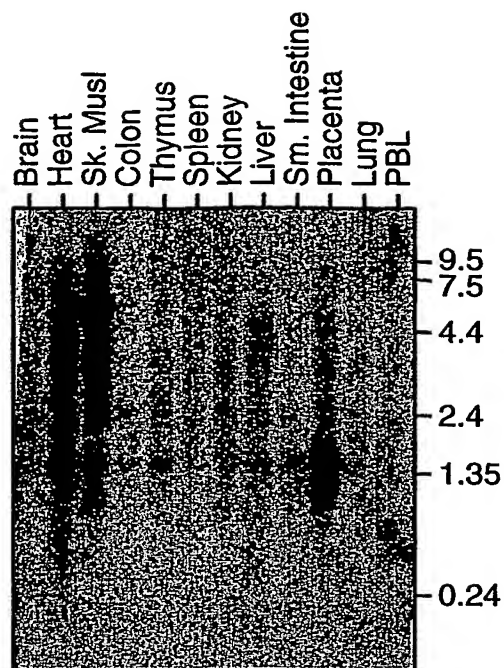
human EESWTPNYKQCSWSSLYGIDLGKIAECTFTKMRNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGGLPIEAIIYLDQGSPEMNSTINIHRTSSVE  
 mouse EESWTPNYKQCSWSSLYGIDLGKIAECTFTKMRNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGGLPIEAIIYLDQGSPEMNSTINIHRTSSVE  
 rice\_fish EEPWKPNYKQCAWNSLYGIDLGKIACTFTKLRSEALRVLFTGSLRLKCKEACCCQRWYFTFDGAECTGGLPIESIIYLDQGSPEMNSTINIHRTSSVE  
 abra\_fish EEPWKPNYKQCAWNSLYGIDLGKIACTFTKQSDSALRVLFTGSLRLKCKTACCQRWYFTFNGAECTGGLPIESIVYLDQGSPEMNSTINIHRTSTVE  
 chicken EESWTPNYKQCSWSSLYGIDLGKIAECTFTKMRNSALRVLFSGSLRLKCRSACCQRWYFTFNGAECAGPLPIEAIIYLDQGSPEMNSTINIHRTSSVE  
 nsensus EESWtPN%KQCSWSSLYGIDLGKIA#CTFTKRS#SALRVLFSGSLRLKCr.ACCQRWYFTF#GAEC.GPLP!EaI!YL#QGSPE\$NSTINIHRTSSVE

FIG.\_1

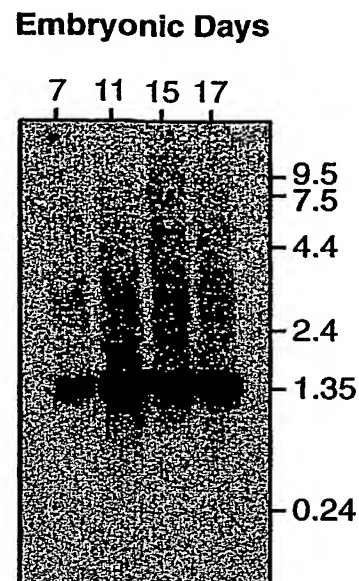
human GLCEGIGAGLVDAIWWGTCSDPYKGDASTGWNVSRIIEELPK  
 mouse GLCEGIGAGLVDAIWWGTCSDPYKGDASTGWNVSRIIEELPK  
 rice\_fish GLCEGIGAGLVDAIWWGTCDYPRGDASTGWNVSRIIEELPK  
 abra\_fish GLCEGIGAGLVDAIWWGTCDYPRGDASTGWNVSRIIEELPK  
 chicken GLCEGINAGLVDAIWWGTCSDPYPRGDASTGWNVSRIIEELPK  
 nsensus GLCEGI.AGLVDIaIWWGTCSDPYPRGDASTGWNVSRIIEELPK

MRPQGAASPQRLRGLLLLLLLQLPAPSSASEIPKQKQALRQREVVDLYNG  
 60 70 80 90 100  
 MCLQGPAGVPGRDGSPGANGIPGTPGIPGRDGNPGKGEKGECLRESFEESWTPNY  
 110 120 130 140 150  
 KQCSWSSLYGIDLGKIAECTFTKMRNSALRVLFSGSLRLKCRNACCQRWYF  
 50 170 180 190 200 210  
 TFNGAECGGLPIEAIIYLDQGSPEMNSTINIHRTSSVEGLCEGIGAGLVDA  
 220 230 240  
 IWVGTCSDPYKGDASTGWNVSRIIEELPK

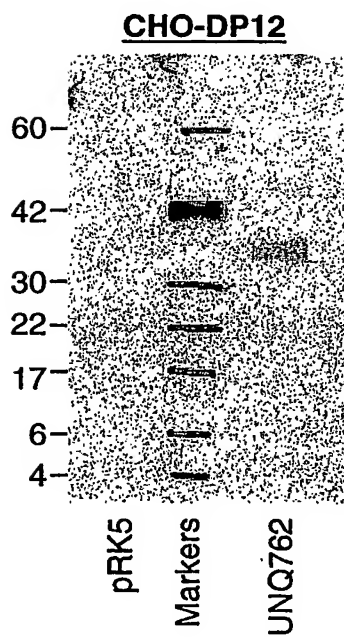
FIG.\_2



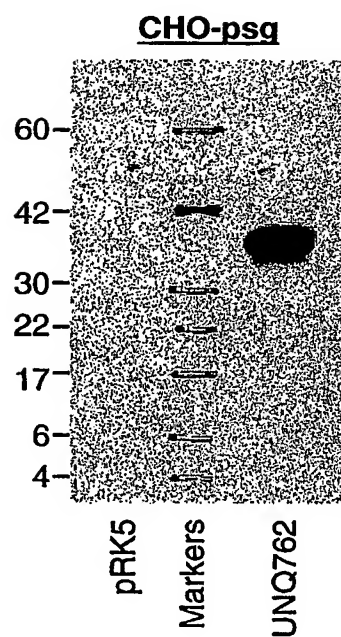
**FIG.\_3A**



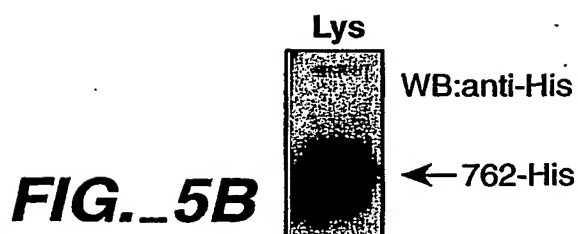
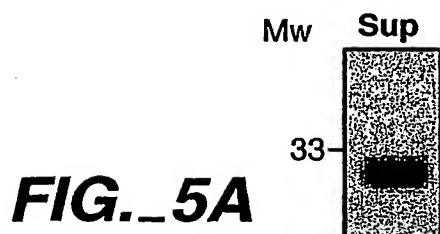
**FIG.\_3B**

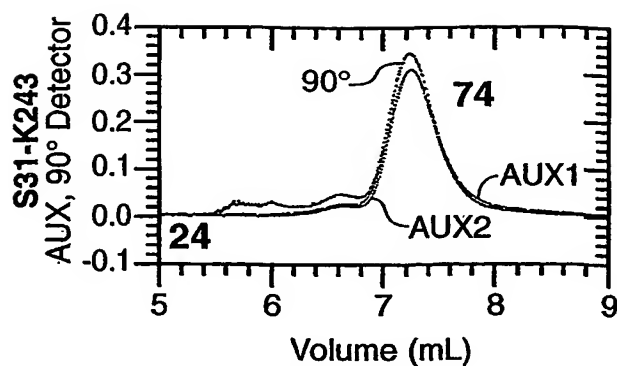


**FIG.\_4A**

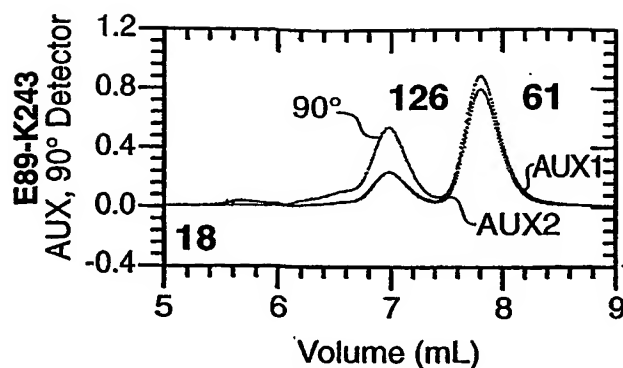


**FIG.\_4B**

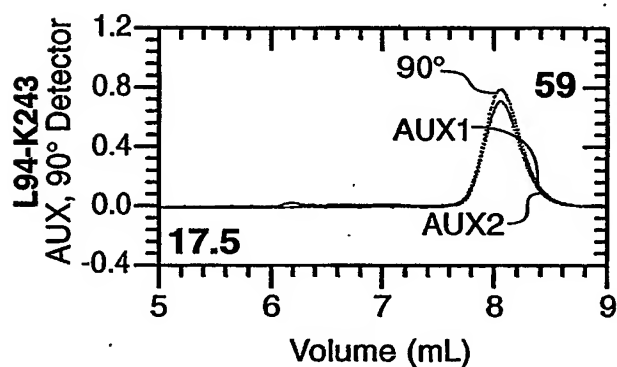




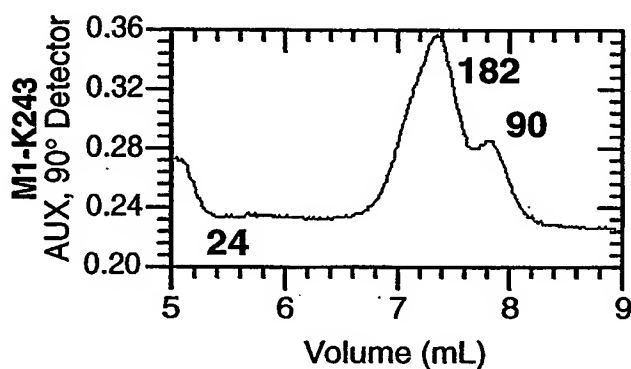
**FIG.\_6A**



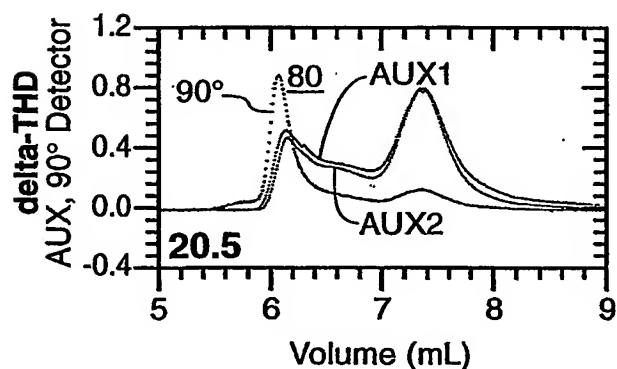
**FIG.\_6B**



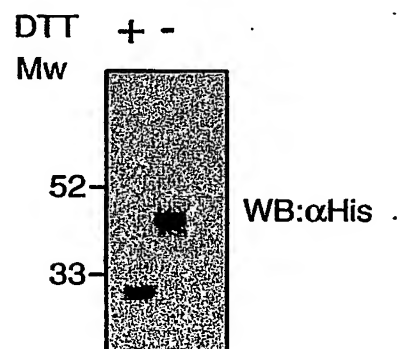
**FIG.\_6C**



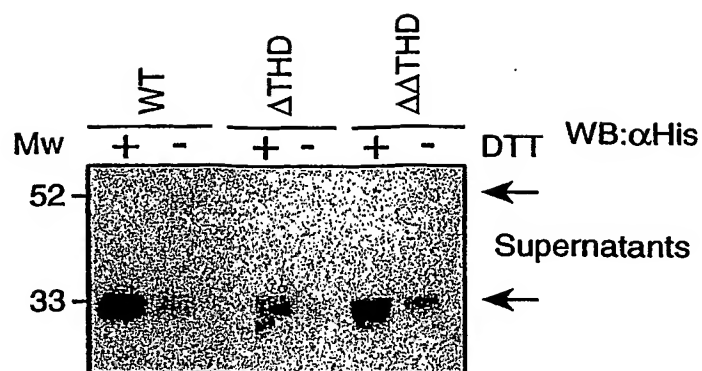
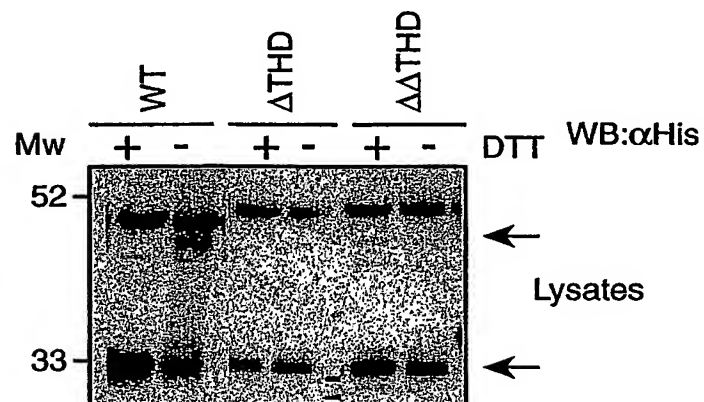
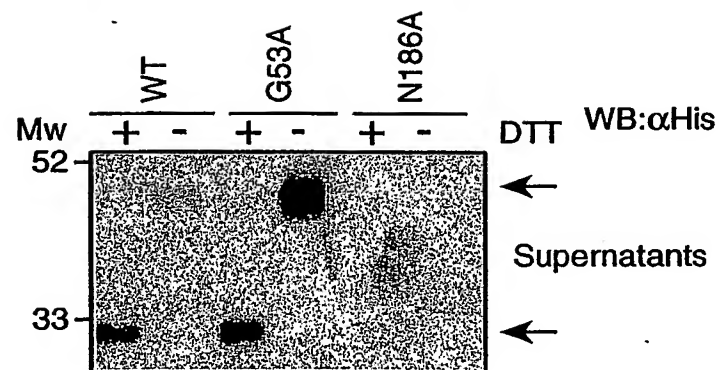
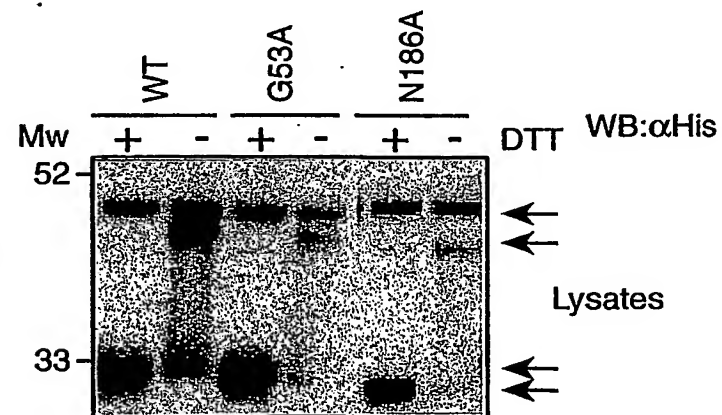
**FIG.\_7A**



**FIG.\_7B**

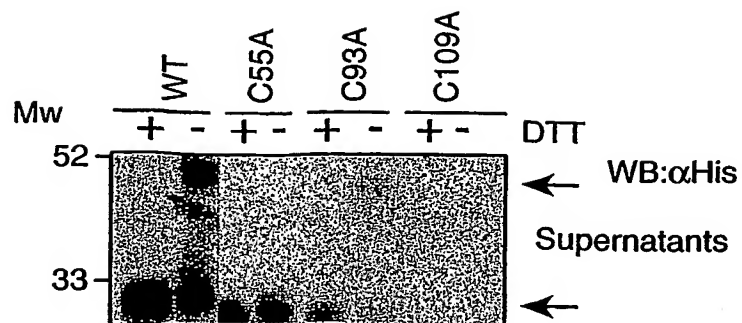


**FIG.\_7C**

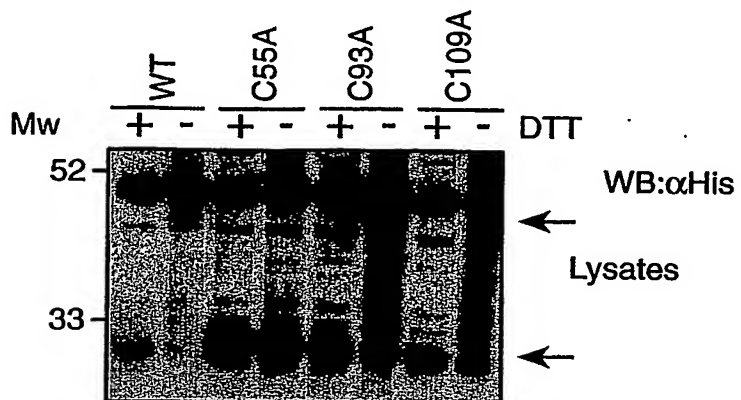
**FIG.\_8A****FIG.\_8B****FIG.\_9A****FIG.\_9B**



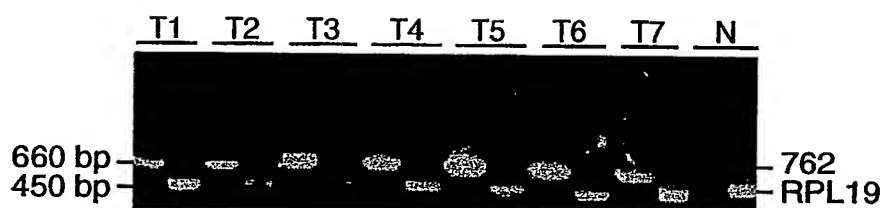
**FIG.\_10A**

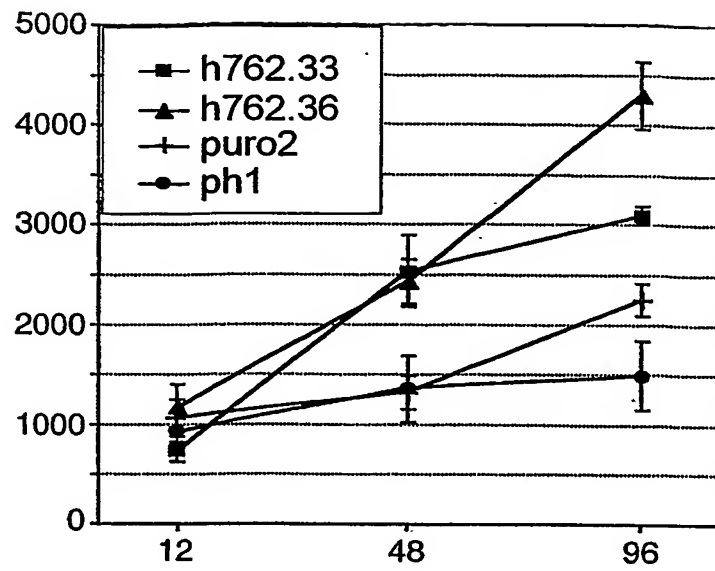
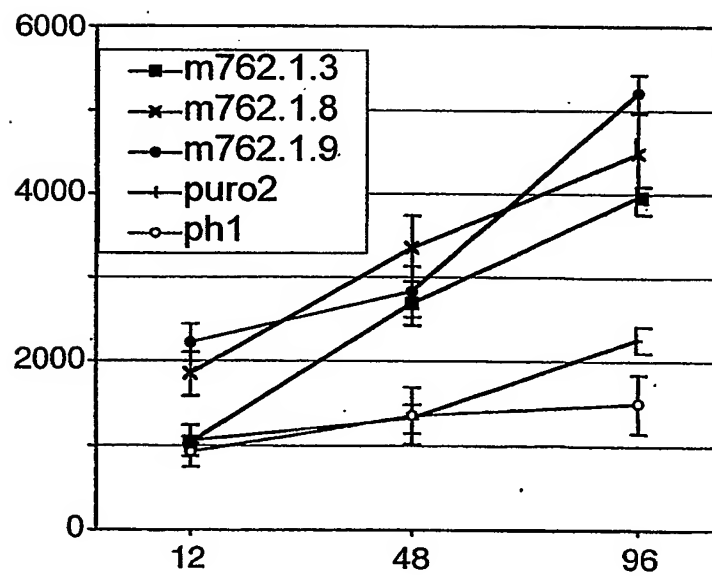


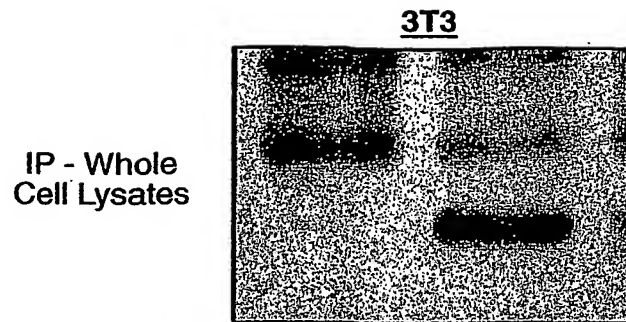
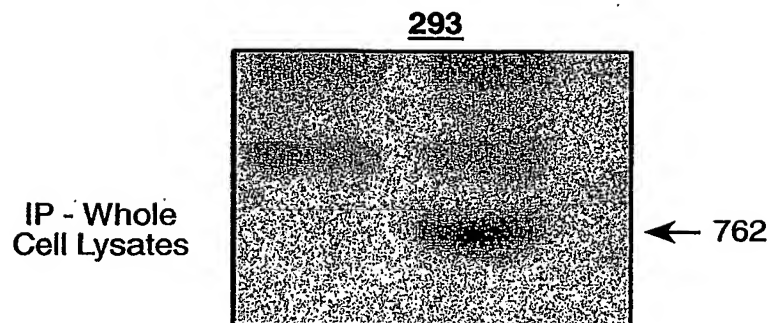
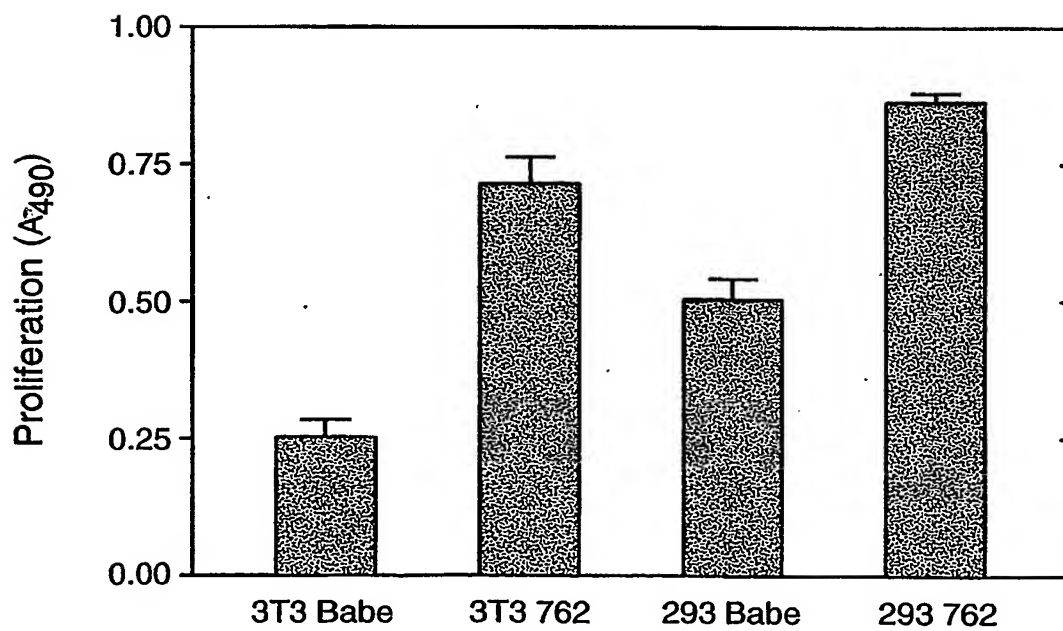
**FIG.\_10B**

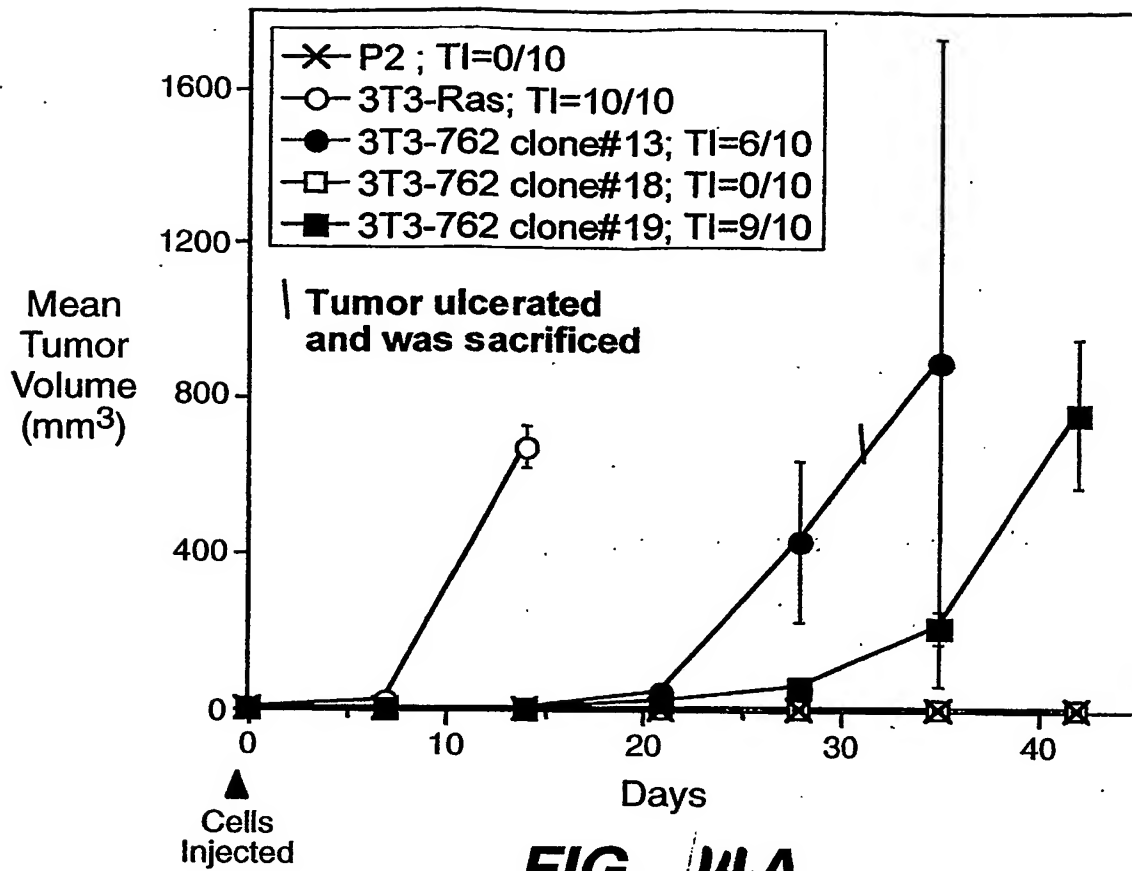
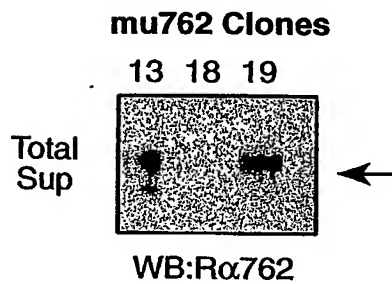
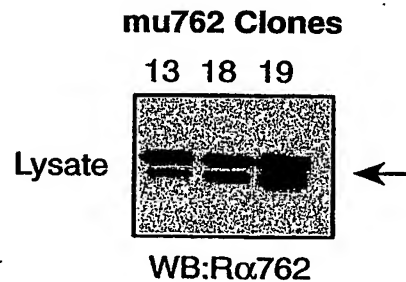


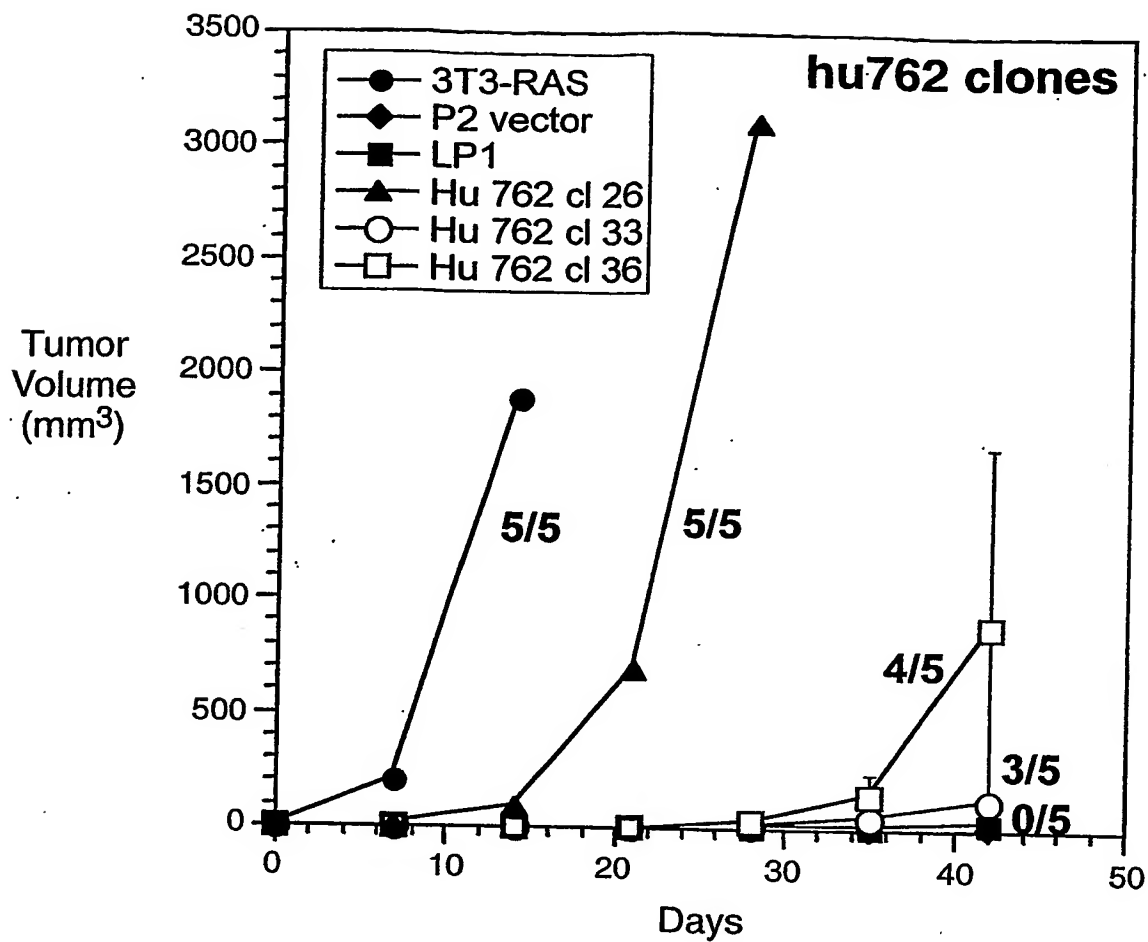
**FIG.\_11**

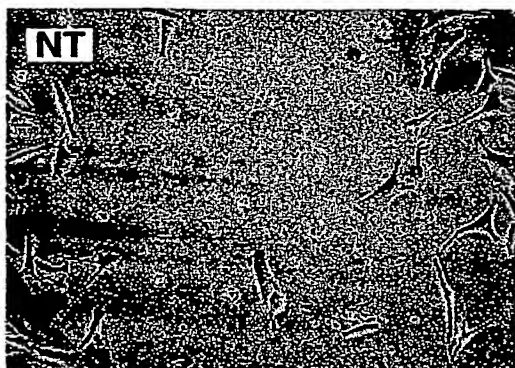


**FIG. 12A****FIG. 12B**

**FIG. 13A****FIG. 13B****FIG. 13C**

**FIG. 14A****FIG. 14B****FIG. 14C**

**FIG. 15**



**FIG. 16A**



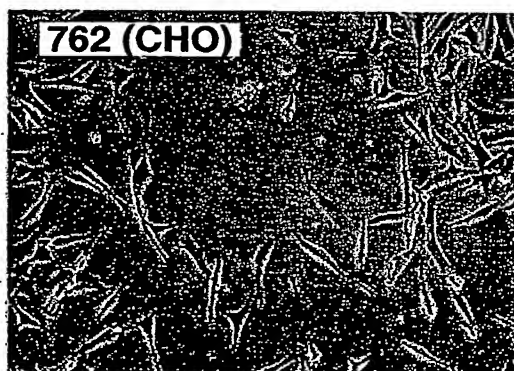
**FIG. 16C**



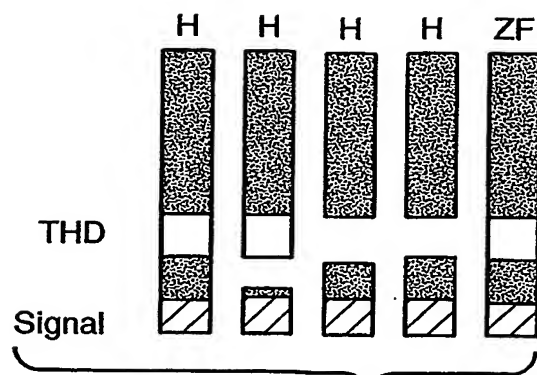
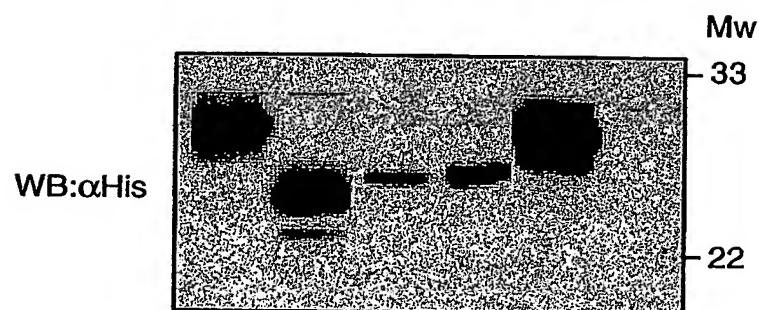
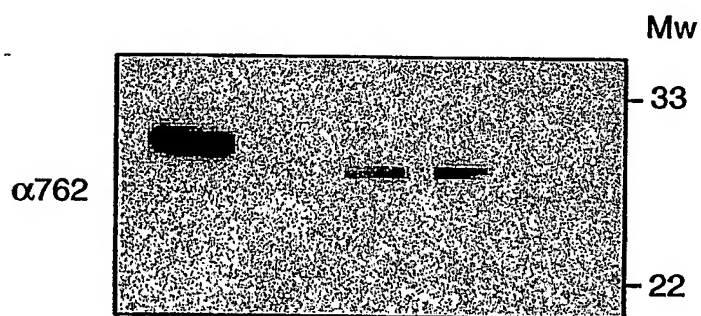
**FIG. 16B**



**FIG. 16D**



**FIG. 16E**

**FIG. 17A****FIG. 17B****FIG. 17C**

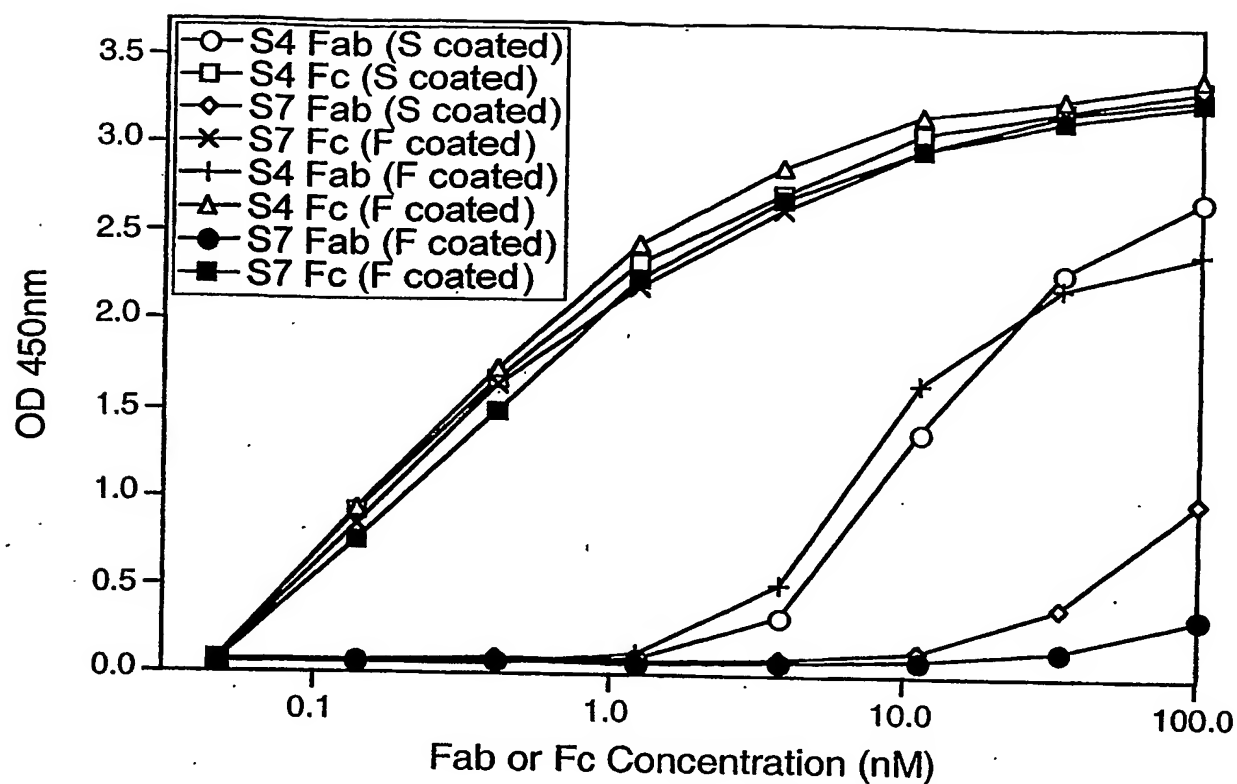
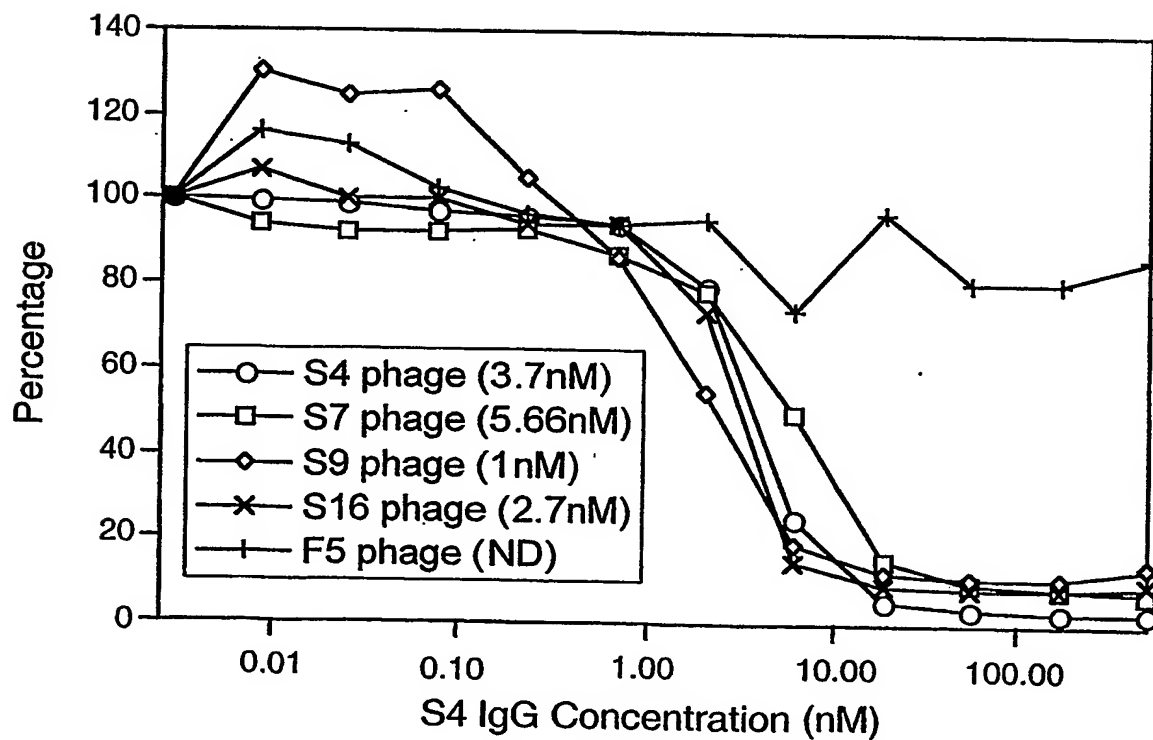
H1										H2										H3										Name	
8	29	30	31	32	33	49	50	51	52	52a	53	54	55	56	57	58	92	93	94	95	96	97	98	99	100	100a	100b	100c	101	102	
I	S	G	S	D	D	G	R	I	S	P	Y	G	G	N	T	N	C	A	R	V	G	G	L	K	L	L	-	F	D	Y	S7
I	T	N	S	D	D	A	T	I	Y	P	Y	G	G	Y	T	Y	C	A	R	G	G	M	D	G	Y	V	M	D	D	Y	S16
I	N	N	Y	D	D	G	Y	I	S	P	P	S	G	A	T	Y	C	A	R	M	V	G	M	R	R	G	V	M	D	Y	F5
I	N	N	Y	D	D	G	Y	I	S	P	P	S	G	A	T	Y	C	A	R	M	V	G	M	R	R	G	V	M	D	Y	F6
I	S	G	S	W	W	A	W	I	A	P	Y	S	G	A	T	D	C	A	R	E	G	G	L	Y	W	V	-	F	D	Y	S4
I	S	N	Y	G	G	G	R	I	S	P	S	N	G	S	T	Y	C	A	K	C	S	V	R	-	-	-	-	F	A	Y	S9
I	S	G	S	W	W	A	W	I	A	P	Y	S	G	A	T	D	C	A	R	E	G	G	L	Y	W	V	-	F	D	Y	F13
I	S	G	S	W	W	A	W	I	A	P	Y	S	G	A	T	D	C	A	R	E	G	G	L	Y	W	V	-	F	D	Y	F47

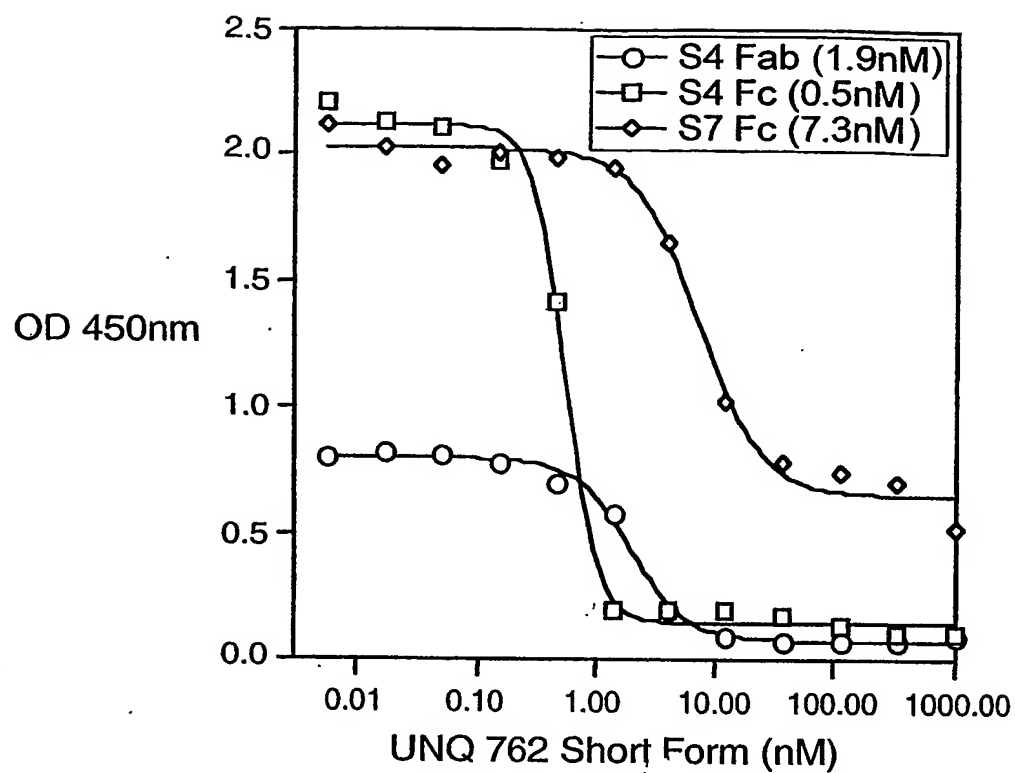
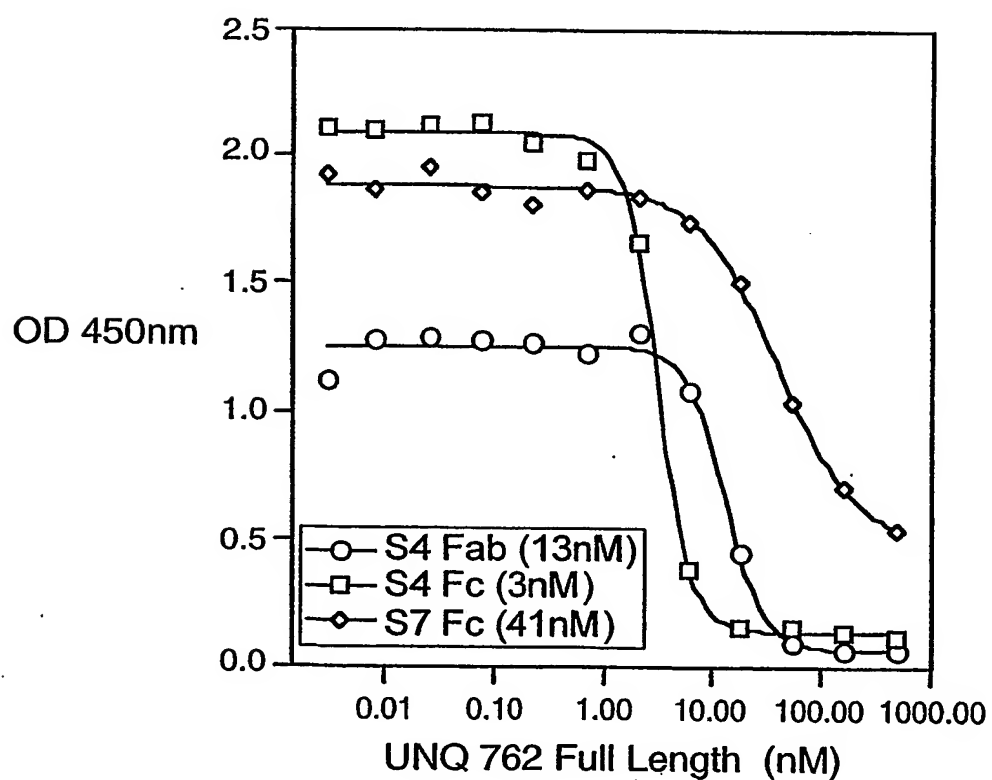
FIG. 18

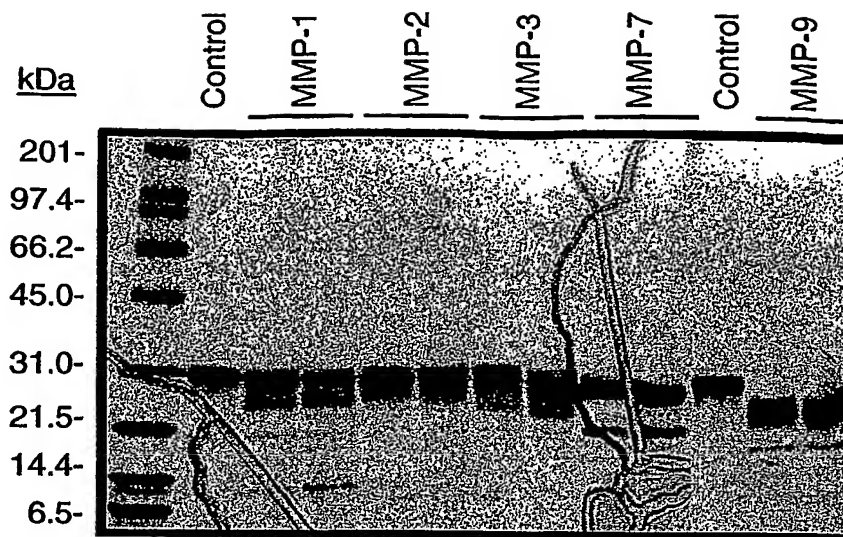
Phage			Fab			IgG		
762 S/S	762 F/F		762 S/S	762 F/S	762 F/F	762 S/S	762 F/F	
3nM	0.9nM		3.6nM (1.9nM)	32nM	13.4nM	0.5nM	3.1nM	
762 S/S	762 F/F		762 S/S	762 F/S	762 F/F	762 S/S	762 F/F	
35nM	2.7nM		113nM	57nM	n/a	7.3nM	41nM	
S4								
S7								

FIG. 19

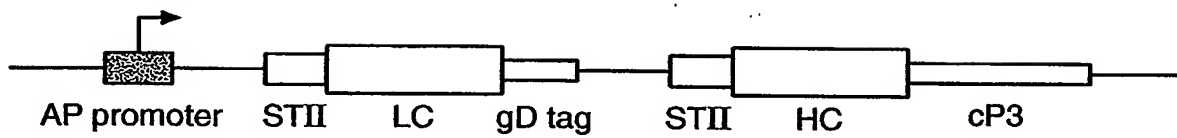


**FIG. 19****FIG. 20**

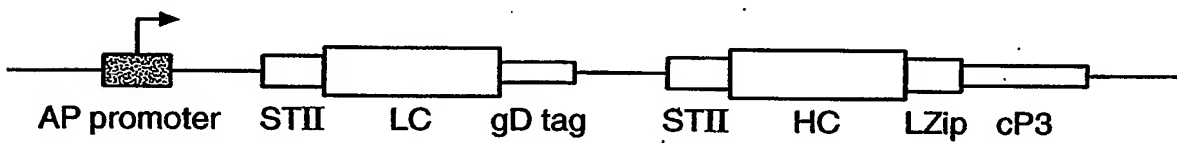
**FIG. 20 A.****FIG. 20 B.**



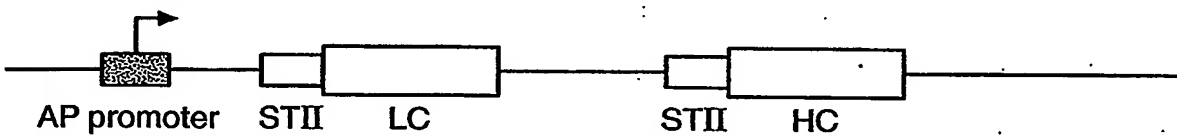
**FIG. 23**



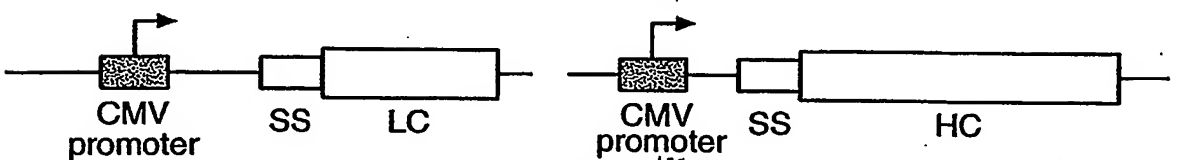
**FIG. 24 A**



**FIG. 24 B**



**FIG. 24 C**



**FIG. 24 D**

```

1 GAATTCAACT TCTCCATACT TTGGATAAGG AATACAGAC ATGAAAAATC TCATTGCTGA GTTGTATTAT AAGCTTGCCC AAAAAAGA AGAGTCGAAT
CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGTCG TACTTTTAG AGTAACGACT CAACAATAA TTCGAACGGG TTTTTCITCT TCTCAGCTTA

101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACACAGG GTTGATTGAT CAGGTAGAGG
CTTGACACAC GCGTCCATCT TCGAAACCTC TAATAGCAGT GAGGTACGA AGCGTATAC CGCGTTTAC TGGTTGTCGC CAACTAACTA GTCCATCTCC

201 GGGCGCTGTA CGAGGTAAG CCGGATGCCA GCATTCTGTA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA
CCCGCGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGAGC CGCTAATGCA TTTTCTCAAT AACTTCGTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTCAACA GCTGTCATAA AGTTGTCAGG GCGGAGACTT ATAGTCGCTT TGTTTTATT TTTTAATGTA TTTGTAACATA GTACGCAAGT
TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAAAATAA AAAATTACAT AAACATTGAT CATGCGTTCA

401 TCACGTAAAA AGGGTATGTA GAGGTGAGG TGATTTTATG AAAAAAATA TCGCATTTCT TCTTGCACTC ATGTTCTGTTT TTTTCTATTGC TACAAATGCC
AGTGCATTTT TCCCATACAT CTCCAACCTC ACTAAATAC TTTTCTTAT AGCGTAAAGA AGAAGCTAGA TACAAGCAAA AAAGATAACG ATGTTTACGG
1 M K K N I A F L L A S M F V F S I A T N A
^start of stII signal sequence
^met

501 TATGCAGATA TCCAGATGAC CCAGTCCCCG AGCTCCCTGT CCGCCCTGTGT GGGCGATAGG GTCACCATCA CCTGCCGTGC CAGTCAGGAT GTCTCCACTG
ATACGTCTAT AGGTCTACTG GGTCAAGGGC TCCAGGGACA GCGGGAGACA CCGGTATPCC CAGTGGTAGT GGACGGCAGG GTCAGTCCCTA CACAGGTGAC
22 Y A D I Q M T Q S P S S L S A S V G D R V T I T C R A S Q D V S T A
^start of light chain ^CDR-L1

601 CTGTAGCCTG GTATCAACAG AACCCAGGAA AAGCTCCGAA GCCTCTGATT TACTCGGCAT CCTTCCCTCA CTCTGGAGTC CCTTCTCGCT TCTCTGGTAG
GACATCGGAC CATAGTTGTC TTTGGTCCCTT TTCGAGGCTT CGAAGACTAA ATGAGCGGTA GGAAGGAGAT GAGACCTCAG GGAAGAGCGA AGAGACCATC
56 V A W Y Q Q K P G K A P K L L I Y S A S F L Y S G V P S R F S G S
^CDR-L2

701 CGGTCCGGG ACGGATTICA CTCTGACCAT CAGCAGTCTG CAGCCGGAAG ACTTCGCAAC TTATTACTGT CAGCAATCTT ATACTACTCC TCCCACGTTT
GCCAAGGCCC TGCCTAAAGT GAGACTGGTA GTCGTCAGAC GTCGGCCTTC TGAAGCGTTG AATAATGACA GTCGTTAGAA TATGATGAGG AGGTTGCAAG
89 G S G T D F T L T I S S L Q P E D F A T Y Y C Q Q S Y T T P P T F
^CDR-L3

```

**FIG. 25A**

```

301 GGACAGGGTA CCAAGGTGGA GATCAAAACGA ACTGTGGGCTG CACCATCTGT CTTCATCTTC CCGCCATCTG ATGAGCAGTT GAAATCTGGA ACTGCCCTCTG
    CCTGTCCCAT GGTTCACCT CTAGTTTGCT TGACACCGAC GTGGTAGACA GAAGTAGAAG GCGGTAGAC TACTCTCAA CTTTAGACCT TGACGGAGAC
122 G Q G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S V
301 TTGTGTGCT GCTGAATAAC TTCTATCCCA GAGAGGCCAA AGTACAGTGG AAGGTGGATA AGCCCTCCA ATCGGGTAAC TCCCAGGAGA GTGTACACAGA
    AACACACGGA CGACTTATTG AAGATAGGTT CTCTCCGGTT TCATGTCCACC TTCCACCTAT TCGGGGAGGT TAGCCCATG AGGCTCTCT CACAGTGTCT
156 V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E
301 GCAGGACAGC AAGGACAGCA CCTACAGCCT CAGCAGCACC CTGACGCTGA GCAAAGCAGA CTACGAGAAA CACAAAGTCT ACGCTGCCA AGTCACCCAT
    CGTCCTGTCG TTCCTGTGCT GGATGTCGGA GTCTGCTGG GACTGCGACT CGTTTCGTCT GATGCTCTTT GTGTTTCAGA TCGGGACGCT TCAGTGGGTA
189 Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H
301 CAGGGCCTGA GCTCGCCCGT CACAAAGAGC TTCAACAGGG GAGAGTGTGG TGCCAGCTCC GGTATGGCTG ATCCGAACCG TTTCCGCGGT AAGGACCTGG
    GTCCCGGACT CGAGCGGGCA GTGTTTCTCG AAGTTGTCCC CTCTCACACC ACGGTGAGG CCATACCGAC TAGGCTTGGC AAAGGCGCCA TTCTTGGACC
222 Q G L S S P V T K S F N R G E C G A S S G M A D P N R F R G K D L A
    ^end of light chain, start of gD tag
17/75
01 CATAACTCGA GGCTGATCCT CTACGCCGGA CGCATCGTGG CCCTAGTACG CAAGTTCACG TAAAAAGGGT AACTAGAGGT TGAGGTGATT TTATGAAAAA
    GTATTGAGCT CCGACTAGGA GATCGGCGCT GCGTAGCACC GGGATCATGC GTTCAAGTGC ATTTTTCCTCA TTGATCTCCA ACTCCACTAA AATACTTTTT
156 O
23 M K K
    ^start of stII
01 GAATATCGA TTTCTTCTTG CATCTATGTT CGTTTTTCTT ATTGCTACAA ACGCGTACG TGAGGTTCAG CTGTGGAGT CTGGCGGTGG CCTGGTGCAG
    CTTATAGCGT AAAGAAGAAC GTAGATACAA GCAGGAGGCA AGTTGTAATT TCTGTGGATA TATGTGACCC ACCAGTCCG GGGCCCATTC CCGGACCTTA
20 N I A F L L A S M F V F S I A T N A Y A E V Q L V E S G G L V Q
    ^start of heavy chain
01 CCAGGGGGCT CACTCCGTTT GTCTGTGCA GCTTCTGGCT TCAACATTAA AGACACCTAT ATACACTGG TCGTTCAGG CCGGGTAAG GGCCTGGAAT
    GGTCCCCCGA GTGAGGCAAA CAGGACACGT CGAAGACCGA AGTTGTAATT TCTGTGGATA TATGTGACCC ACCAGTCCG GGGCCCATTC CCGGACCTTA
14 P G G S L R L S C A A S G F N I K D T Y I H W V R Q A P G K G L E W
    ^CDR-H1

```

FIG. 25B

1501 GGGTTGCAAG GATTTATCCT AGGAATGGTT AATAAGATA TGCCGATAGC GTCAAGGCGC GTTTCACAT AAGCGCAGAC ACATCCAAA ACACAGCCTA  
 CCCAACGTTT CTAATAAGGA TGCTTACCAG CAGTTCCCGG CAAAGTGATA TTCCGGCTCG TGTAGGTTTT TGTGTCGGAT  
 48 V A R I Y P T N G Y T R Y A D S V K G R F T I S A D T S K N T A Y  
 ^CDR-H2  
 1601 CCTACAAATG AACAGCTTAA GAGCTGAGGA CACTGCCGTC TATATATGTA GCCGCTGGGG AGGGACGGC TTCTATGCTA TGGACTACTG GGTCAAGGA  
 GGATGTTTAC TTGTCCGAAT CTGCACTCCT GTGACGGCAG AATAAATCAT CGCGACCCC TCCCCTGGG AAGATACGAT ACCTGATGAC CCCAGTTTCT  
 81 L Q - M N S L R A E D T A V Y Y C S R W G G D G F Y A M D Y W G Q G  
 ^CDR-H3  
 1701 AACTAGTCA CCGTCTCCTC GGCCTCCACC AAGGCCCAT CCGTCTTCCC CTTGGCACCC TCCTCCAAGA GCACCTCTGG GGCACACGG GCCCTGGGCT  
 TGTGATCAGT GGCAGAGGAG CCGGAGGTGG TTCCCGGGTA GCCAGAAGG GACCGTGGG AGGAGTTCT CTTGGAGACC CCCGTGTGCG CGGGACCCGA  
 114 T L V T V S S A S T K G P S V F P L A P S S K S T S G G T A A L G C  
 1801 GCCTGGTCAA GGACTACTTC CCGAACCAGG TGACGGTGC GTGGAATCA GCGGCCCTGA CCAGGGCGT GCACACCTTC CCGGCTGTCC TACAGTCTCT  
 CGGACCAAGT CCTGATGAG GGGCTTGGCC ACTGCCACAG CACCTTGAGT CCGCGGGACT GGTCCCGCA CGTGTGAAG GCGGACAGG ATGTCAGGAG  
 148 L V K D Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S S  
 1901 AGGACTCTAC TCCCTCAGCA GCGTGTGAC GGTGCCCTCC AGCAGCTGG GCACCCAGAC CTACATCTGC AACCTGAATC ACAAGCCAG CAACACCAAG  
 TCCTGAGATG AGGAGTCGT CGCACCCTG GCACGGGAGG TCGTCAACC CCGTGGTCTG GATGTAGACG TTGCACTTAG TGTTCGGTC GTTGTGTTTC  
 181 G L Y S L S S V V T V P S S S L G T Q T Y I C N V N H K P S N T K  
 2001 GTCGACAAGA AAGTTGAGCC CAAATCTTGT GACAAAATC ACCTCAGTGG CCGTGGCTCT GTTCCGGTG ATTTTGATTA TGAAGAATG GCAAACGCTA  
 CAGCTGTCT TTCAACTCGG GTTTAGAACA CTGTTTGTAG TGGAGTCACC GCCACCGAGA CCAAGGCCAC TAAACTAAT ACTTTCTAC CGTTTGGGAT  
 214 V D K K V E P K S C D K T H L S G G S G S G D F D Y E K M A N A N  
 ^end of heavy chain  
 ^start of gene III coat protein (267-end)  
 2101 ATAAGGGGGC TATGACCGAA AATGCCGATG AAAACGGCT ACAGCTGAC GCTAAAGGA AACTTGATTC TGTCGCTACT GATTACGGTG CTGCTATCGA  
 TATTCCCCG ATACTGGCTT TTACGGCTAC TTTTGGCGGA TGTCAGACTG CGATTTCCGT TTGAACCTAG ACAGCGATGA CTAATGCCAC GACGATAGCT  
 248 K G A M T E N A D E N A L Q S D A K G K L D S V A T D Y G A A I D

FIG. 25c

2201 TGGTTTCAATT GGTGACGTTT CCGGCCCTTGC TAATGGTAAT GGTGCTACTG GTGATTTTGC TGGCTCTAAT TCCCAATAGG CTCAAAGTCGG TGACGGTGTAT  
 ACCAAAGTAA CCACTGCAAA GGCCGGAACG ATTACCATTA CCACGATGAC CACTAAACG ACCGAGATTA AGGGTTTACC GAGTTTACCC ACTGCCACTA  
 281 G F I G D V S G L A N G N G A T G D F A G S N S Q M A Q V G D G D  
 2301 AATTCACTT TAATGAATAA TTTCCTGCAAA TATTACCTT CCTCCCTCA ATCGGTGAA TGTCGCCCTT TTGTCTTTAG CGTGGGTAAA CCATATGAAT  
 TTAAGTGGAA ATTACTTATT AAAGGCAGTT ATAAATGGAA GGGAGGAGT TAGCCAACCT ACAGCGGAA AACAGAAATC GCGACCATTT GGTATACTTA  
 314 N S P L M N N F R Q Y L P S L P Q S V E C R P F V F S A G K P Y E F  
 2401 TTCTCTATTG TTGTGACAAA ATAACTTAT TCCGTGGTGT CTTTGGCTTT CTTTATATATG TTGCCACCTT TATGTATGTA TTTTCTACGT TTGCTAACAT  
 AAAGATAACT AACACTGTTT TATTGTAATA AGGCACCACA GAACGCAAA GAAATATATC AACGCTGGA ATACATACAT AAAAGATGCA AACGATTGTA  
 348 S I D C D K I N L F R G V F A F L L Y V A T F M Y V F S T F A N I  
 2501 ACTGCGTAAT AAGAGTCTT AATCATGCA GTTCTTTTGG CTAGCGCCG CCTATACCTT GTCTGCCTCC CCGCGTTGG TCGCGGTGCA TGGAGCCGGG  
 TGACGCATTA TTCTCAGAA TTAGTACGGT CAAGAAAACC GATCGCGCG GATATGGA CAGACGGAGG GCGCAACGC AGCGCCACGT ACCTCGGGCC  
 381 L R N K E S O  
 2601 CCACCTCGAC CTGAATGAA GCCGGCGGCA CCTCGCTAAC GGATTCACCA CTCCAAGAAT TGGAGCCAAT CAATTCTTGC GGAGAACTGT GAATGCGCAA  
 GGTGGAGTGC GACTTACCTT CGGCGGCCGT GGAGCGATTG CCTAAGTGGT GAGGTTCTTA ACCTCGGTTA GTTAAGAAGC CCTCTTGACA CTTACGCGTT  
 2701 ACCAACCTT GGCAGAACAT ATCCATCGCG TCCGCCATCT CCAGCAGCG CACGCGGCG ATCTCGGCA GCGTTGGGT CTTGGCCACGG GTGCGCATGA  
 TGGTTGGGAA CCGTCTTGTA TAGGTAGCGC AGGCGGTAGA GGTCTGTGCG GTGCGCGCG TAGAGCCCGT CGCAACCCAG GACCGGTGCC CACGCGTACT  
 2801 TCGTCTCCT GTCGTTGAGG ACCCGGCTAG GCTGGCGGG TTGCCTTACT GGTTAGCAGA ATGAATCACC GATACGCGAG CGAACGTGAA GCGACTGCTG  
 AGCAGGAGA CAGCAACTCC TGGGCCGATC CGACCGCCCC AACGGAATGA CCAATGCTCT TACTTAGTGG CTATGCGCTC GCTTGACITT CGCTGACGAC  
 2901 CTGCAAAACG TCTGCGACCT GAGCAACAC ATGAATGGTC TTCGGTTTCC GTGTTTCGTA AAGTCTGGAA ACGCGGAAGT CAGCGCCCTG CACCATATG  
 GACGTTTTCG AGACGCTGGA CTCGTTGTTG TACTTACCAG AAGCCAAGG CACAAAGCAT TTCAGACCTT TCGCCCTTCA GTCGCGGAC GTGGTAATAC  
 3001 TTCCGGATCT GCATCGCAGG ATGCTGCTGG CTACCCCTG GAACACCTAC ATCTGTATTA ACGAAGCGCT GGCATTGACC CTGAGTGAAT TTTCTCTGTT  
 AAGGCCTAGA CGTAGCGTCC TAGCAGGACC GATGGGACAC CTTGTGGATG TAGACATAAT TGCTTCGCGA CGTAACTGG GACTCACTAA AAAGAGACCA

**FIG. 25D**

101 CCGCGCCGCAT CCATACCGCC AGTTGTTTAC CCTCACAAACG TTCCAGTAAC CCGGCATGTT CATCATCAGT AACCCGTATC GTGAGCATCC TCTCTCGTTT  
GGCGCGCGTA GGTATGGCGG TCACACAAATG GGAGTGTTGC AAGGTCATTG GCGGTACAA GTAGTAGTCA TTGGGCATAG CACTCGTAGG AGAGAGCAAA  
201 CATCGGTATC ATTACCCCA TGAACAGAAA TTCCCCCTTA CACGGAGGCA TCAAGTGACC AACAGGAAA AACCCGCCCT TAACATGGCC CGCTTTATCA  
GTAGCCATAG TAATGGGGGT ACTTGCTCTTT AAGGGGGAAT GTGCCTCCGT AGTTCACCTGG TTGTCTCTTT TTTCGGGGA ATTGTACCGG GCGAAATAGT  
301 GAAGCCAGAC ATTAACGCTT CTGGAGAAAC TCAACGAGCT GGACGGGAT GAACAGGAG ACATCTGTGA ATCGTTTAC GACCAGCTG ATGAGCTTTA  
CTTCGGTCTG TAATTGGGAA GACCTCTTTG AGTTGCTGA CCTGCGCCTA CTGTCCGTC TGTAGACACT TAGCGAAGTG CTGGTCCGAC TACTCGAAAT  
401 CCGCAGGATC CGGAAATTGT AAACGTTAAT ATTTTGTAA AATTCGCCGT AAATTTTGT TAAATCAGCT CATTTTTTAA CCAATAGGCC GAAATCGGCA  
GGCGTCCCTAG GCCTTTAACA TTGCAATTA TAAACAAT TTAAGCGCAA TTAAACAACA ATTTAGTGA GTAAAAAATT GGTATCCGG CTTTAGCCGT  
501 AAATCCCCTTA TAAATCAAAA GAATAGACCG AGATAGGGTT GAGTGTTGTT CCAGTTTGA ACAAGAGTCC ACTATTAAG AACGTGGACT CCAACGTCAA  
TTTAGGGAAT ATTTAGTTT CTATCTGGC TCTATCCAA CTCACACAA GGTCAAACCT TGTCTCAGG TGATAATTTC TTGCACCTGA GGTTCAGTT  
01 AGGGCGAAA ACCGTCTATC AGGGCTATGG CCCACTACGT GAACCATCAC CCTAATFCAAG TTTTITGGGG TCGAGGTGCC GTAAAGCACT AAATCGGAAC  
TCCCGCTTTT TGGCAGATAG TCCCGATACC GGTGATGCA CTGTGTAGTG GGATTAGTTC AAAAAACCC AGCTCCACGG CATTTCTGTA TTTAGCCTTG  
701 CCTAAAGGA GCGCCCGATT TAGAGCTTGA CCGGGAAGC CCGGAACGT GCGGAGAAG GAAGGAAG AAGCGAAAG AGCGGGCGCT AGGGCGCTGG  
GGATTCCCT CCGGGGCTAA ATCTCGAAT ATCTCGAAT CCCCCTTTCG GCGCTTTC CCGCTCTTC CTTCCTTTC TTTCCTTTC TCGCCCGCA TCCCGCGACC  
801 CAAGTGTAGC GGTACGCTG CCGGTAACCA CCACACCCG CCGCTTAAT GCGCCGTAC AGGGCGCTC CCGATCCTGC CTCGGCGGTT TCGGTGATGA  
GTTACATCG CCAGTCCGAC GCGCATTTGT GGTGTGGCG GCGGAATTA CCGGCGGATG TCCCGCGCAG GCCTAGGAGG GAGCGCGCAA AGCCACTACT  
901 CCGTGAAAAC CTCTGACACA TGCAGCTGCC GGAGACGCTC ACAGCTTGT TGTAAAGCGA TGCCGGGAGC AGACAAGCC GTACGGCGG GTACGGCGGT  
GCCACTTTG GAGACTGTGT ACGTCCAGG CCTCTGCCAG TGTCGAACAG ACATTCGCCT ACGGCCCTC TCTGTTCGG CAGTCCCGG CAGTCGCCCCA  
101 GTTGGCGGGT GTCGGGGCG AGCCATGACC CAGTCACGTA GCGATAGCG AGTGATATCT GGTAACTA TCGGGCATCA GAGCAGATTG TACTGAGAGT  
CAACCGCCCCA CAGCCCCGG TCGGTACTGG GTCAGTGCAT CGCTATCGC TCACATATGA CCGAATTGAT ACGCGTAGT CTCGTCTAAC ATGACTCTCA

20/75

FIG. 25E



4101 GCACCATATG CGGTGTGAAA TACCGCACAG ATCGGTAAGG AGAAATACC GCATCAGGCG CTCTTCCGCT TCCTCGCTCA CTGACTCGCT GCGCTCGGTC  
 CGTGGTATAC GCCACACTTT ATGGCGGTGC TACGCATTCC TCTTTTATGG CGTAGTCCGC GAGAAAGCGA AGGAGCGAGT GACTGAGCGA CGCGAGCCAG  
  
 4201 GTTCGGCTGC GCGGAGCGGT ATCAGCTCAC TCAAAGGCGG TAATACGGTT ATCCACAGAA TCAGGGGATA AGCAGGAAA GAACATGTGA GCAAAAGGCC  
 CAAGCCGACG CCGCTCGCCA TAGTCGAGTG AGTTTCGGCC ATTATGCCAA TAGGTGTCTT AGTCCCTAT TCGTTCCTTT CTGTACACT CGTTTCCGG  
  
 4301 AGCAAAAGGC CAGGAACCGT AAAAAGGCGG CGTTGCTGGC GTTTTTCAT AGGCTCCGCC CCCCTGACGA GCATCACAAA AATCGACGCT CAAGTCAGAG  
 TCGTTTTCCG GTCCCTGGCA TTTTTCGGC GCAACGACCG CAAAAGGTA TCCGAGGCGG GGGGACTGCT CGTAGTGTTT TTAGCTCGA GTTCAGTCTC  
  
 4401 GTGGCGAAC CCGACAGGAC TATAAGATA CCAGGCGTTT CCCCTGGAA GCTCCCTCGT GCGCTCTCCT GTTCCGACCC TCGCGCTTAC CGGATACCTG  
 CACCGCTTTG GGCTGTCTG ATATTCTAT GGTCCGCAA GGGGACCTT CGAGGAGCA CCGGAGGGA CAAGGCTGGG ACGGCGAATG GCCTATGGAC  
  
 4501 TCCGCTTTC TCCCTTCGGG AAGCGTGGG CTTTCTCATA GCTCACGCTG TAGGTATCTC AGTTCGGGT AGGTCTGTCG CTCCAAGCTG GGTGTGTGTC  
 AGCGGGAAG AGGGAAGCCC TTCCGACCGC GAAAGAGTAT CGAGTCCGAC ATCCATAGAG TCAAGCCACA TCCAGCAAGC GAGGTTCGAC CCGACACACG  
  
 4601 ACGAACCCC CGTTCAGCCC GACCGCTGG CTTTATCCGG TAATATCGT CTTGAGTCCA ACCCGGTAAG ACACGACTTA TCGCCACTGG CAGCAGCCAC  
 TGCTTGGGG GCAAGTCGGG CTGGCGACG GGAATAGGCC ATTGATAGCA GAATCAGGT TGGGCCATTC TGTGCTGAAT AGCGGTGACC GTCTGTCGGT  
  
 4701 TGGTAACAGG ATTAGCAGAG CGAGGTATGT AGGCGGTGCT ACAGAGTCT TGAAGTGGT GCCTAACACTA GAAGGACAGT ATTTGGTATC  
 ACCATTGTCC TAATCGTCTC GCTCCATACA TCCGCCACGA TGTCTCAAGA ACTTCACCAC CGGATTGATG CCGATGTGAT CTTCCTGTCA TAAACCATAG  
  
 4801 TGGGCTCTGC TGAAGCCAGT TACCTTCGGA AAAAGAGTTG GTAGCTCTTG ATCCGGCAA CAAACCCACCG CTGGTAGCGG TGGTTTTTTT GTTTGCAAGC  
 ACGCGAGACG ACTTCGGTCA ATGGAAGCCT TTTTCTCAAC CATCGAGAAC TAGGCCGTTT GTTTGGTGGC GACCATCGCC ACCAAAAA CAAACGTTTCG  
  
 4901 AGCAGATTAC GCGCAGAAA AAAGGATCTC AAGAAGATCC TTTGATCTTT TCTACGGGT CTGACGCTCA GTGGAACGAA AACTCAGCTT AAGGGATTTT  
 TCGTCTAATG CCGCTCTTTT TTTCTTAGAG TTCTTCTAGG AAATAGAAA AGATGCCCCA GACTGCGAGT CACCTGTGCT TTGAGTGCAA TTCCCTFAAA  
  
 5001 GGTCAATGAGA TTATCAAAA GGATCTTCAC CTAGATCTT TTAAATTAAA AATGAAGTTT TAAATCAATC TAAAGTATAT ATGAGTAAAC TTGGTCTGAC  
 CCAGTACTCT AATAGTTTTT CCTAGAAGTG GATCAGGAA AATTTAATTT TTACTTCAA ATTTAGTTAG ATTTCAATATA TACTCATTTG AACCAGACTG

5101 AGTTACCAAT GCTTAATCAG TGAGGCACCT ATCTCAGCGA TCTGTCTATT TCGTTTCATCC ATAGTTGCCT GACTCCCGCT CGCTAGATA ACTACGATAC  
 TCAATGGTTA CGAATTAGTC ACTCCGTGGA TAGAGTCGCT AGACAGATAA AGCAAGTAGG TATCAACGGA CTGAGGGGCA GCACATCTAT TGATGCTATG  
  
 5201 GGGAGGGCTT ACCATCTGGC CCCAGTGTG CAATGATACC GCGAGACCCA CGCTCACCGG CTCAGATT ATCAGCAATA AACAGCCAG CCGGAAGGGC  
 CCTCCCGAA TGGTAGACCG GGGTCACGAC GTTACTATGG CGCTCTGGT GCGAGTGGC GAGGTCTAAA TAGTCGTTAT TTGGTCGGTC GGCCTTCCCG  
  
 5301 CGAGCGCAGA AGTGGTCCCTG CAACTTTATC CGCTCCCATC CAGTCATTA ATTGTTGCCG GGAAGCTAGA GTAAGTAGTT CGCCAGTTAA TAGTTTGGCG  
 GCTCGGTCT TCACCAGGAC GTTGAATAG GCGGAGGTAG GTGAGATAAT TAACAACGGC CCTTCGATCT CATTCATCAA GCGGTCAATT ATCAAAACGG  
  
 5401 AACGTTGTTG CCATTGCTGC AGGCATCGTG GTGTCACGCT CGTCTGTTGG TATGGCTTCA TTCAGCTCCG GTTCCCAACG ATCAAGGCGA GTTACATGAT  
 TTGCAACAAC GGTACGACG TCCGTAGCAC CACAGTCCGA GCAGCAAAAC ATACCGAAGT AAGTCGAGGC CAAGGGTTGC TAGTTCGGCT CAATGTACTA  
  
 5501 CCCCCATGTT GTGCAAAAAA GCGGTTAGCT CCTTCGGTCC TCCGATCGTT GTCAGAAGTA AGTTGGCCGC AGTGTATCA CTCATGGTTA TGGCAGCACT  
 GGGGGTACAA CACGTTTTTT CGCCAATCGA GGAAGCCAGG AGGCTAGCAA CAGTCTTCAT TCAACCGCG TCACAATAGT GAGTACCAAT ACCGTCGTGA  
  
 5601 GCATAATTCT CTTACTGTCA TGCCATFCCT AGATGCTTT TCTGTGACTG GTGAGTACTC AACCAAGTCA TTCTGAGAAT AGTGTATCG GCGACCGAGT  
 CGTATTAGA GAATGACAGT ACGGTAGGCA TTCTACGAAA AGACACTGAC CACTCATGAG TTGTTTCACT AAGACTCTTA TCACATACGC CGCTGGCTCA  
  
 5701 TGCTCTTGCC CCGCGTCAAC ACGGGATAAT ACCGGCCAC ATAGCAGAAC TTAAAAAGTG CTCATCATTG GAAAAAGTTC TTCGGGGCGA AAACCTCTCA  
 ACGAGAACGG CCCGCAGTTG TGCCCTATTA TGGCGCGGTG TATCGTCTTG AAATTTTCAC GAGTAGTAAC CTTTTGCAAG AAGCCCCGCT TTGTGAGAGTT  
  
 5801 GGATCTTACC GCTGTTGAGA TCCAGTTTGA TGTAAACCCAC TCGTGCACCC AACTGATCTT CAGCATCTTT TACTTTTACC AGCGTTTCTG GGTGAGCAAA  
 CCTAGAAATGG CGACAATCT AGGTCAAGCT ACATTTGGTG AGCAGGTGGG TTGACTAGAA GTCGTAGAAA ATGAAAGTGG TCGCAAGAC CCACCTCGTTT  
  
 5901 AACAGGAAGG CAAAATGCCG CAAAAAAGG AATAAGGGG ACACGGAAAT GTTGAATACT CATACTCTTC CTTTTTCAAT ATTATTGAAG CATTTATCAG  
 TTGTCTTCC GTTTTACGGC GTTTTTTCCC TTATTTCCC TGTTGCCCTTA CAACCTATGA GTATGAGAAG GAAAAAGTTA TAATAACTTC GTAATAATGC  
  
 6001 GGTATTGTC TCATGAGCGG ATACATATTT GAATGTATTT AGAAAAATAA ACAAAATAGG GTTCCGCGCA CATTTCCCG AAAAGTCCCA CCTGACGTCT  
 CCAATAACAG AGTACTCGCC TATGTATAAA CTTACATAAA TCTTTTTATT TGTATTCCC CAAGGCGCT GTAAAGGGC TTTTTCACGGT GGACTGCAGA

101 AAGAAACCAT TATTATCATG ACATTAACTT ATAAAAATAG GCGTATCAG AGCCCTTTC GTCTTCAATA CAGGTAGACC TTTCGTAGAG ATGTACAGTG  
 TTCTTTGGTA ATAAATAGTAC TGTAAATGGA TATTTTATC CGCATAGTGC TCCGGGAAAG CAGAAAGTTAT GTCCATCTGG AAAGCATCTC TACATGTAC

201. AAATCCCCGA AATTATACAC ATGACTGAAG GAAGGAGCT CGTCATTCCC TGCCGGGTTA CGTCACCTAA CATCACTGTT ACTTAAAAA AGTTTCCACT  
 TTTAGGGGCT TTAATATG TGACTGACTTC CTTCCTCGA GCAGTAAGG ACGGCCCAAT GCAGTGGATT GTAGTGACAA TGAATTTTTT TCAAAGGTGA

301 TGACACTTIG ATCCCTGATG GAAAACGCAT AATCTGGAC AGTAGAAAG GCTTCATCAT ATCAAAATGCA AGGTACAAAG AAATAGGGCT TCTGACCTGT  
 ACTGTGAAAC TAGGGACTAC CTTTGTGGTA TTAGACCCCTG TCATCTTCCC CGAAGTAGTA TAGTTTACGT TGCATGTTTC TTATATCCCGA AGACTGGACA

101 GAAGCAACAG TCAATGGGCA TTGTATTAAG ACAAACCTATC TCACACATCG ACAAACCAAT ACAATACAGG TAGACCTTTC GTAGAGATGT ACAGTGAAT  
 CTTCGTGTGC AGTTACCCGT AAACATATTC TGTTGATAG AGTGTGTAGC TGTTTGGTTA TGTTATGTCC ATCTGGAAG CATCTCTACA TGTCACTTTA

501 CCCCAGAAAT ATACACATGA CTGAAGGAAG GGAGCTCGTC ATTCCCTGCC GGGTTACGTC ACCTAACATC ACTGTTACTT TAAAAAAGTT TCCACTTGAC  
 GGGGCTTTAA TATGTGTACT GACTTCTTTC CCTCGAGCAG TAAAGGAGCG CCCAATGCAG TGGATTGTAG TGACAATGAA ATTTTITCAA AGGTGAACTG

01 ACTTTGATCC CTGATGGAAA ACGCATATC TGGACAGTA GAAAGGGCTT CATCATATCA AATGCAACGT ACAAAGAAAT AGGGCTCTG ACCGTGGAAG  
 TGAACACTAGG GACTACCTTT TCGGTATTAG ACCGTGTCAT CTTTCCCGAA GTAGTATAGT TTACGTTGCA TGTTTCTTTA TCCCGAAGAC TGGACACTTC

101 CAACAGTCAA TGGGCATTTG TATAAGACAA ACTATCTCAC ACATCGACAA ACCAATACAA TCTACAGGTA GACCTTTTCGT AGAGATGTAC AGTGAATCC  
 GTTGTAGTT ACCCGTAAAC ATATTCTGTT TGATAGAGTG TGTAGCTGTT TGTTTATGTT AGATGTCCAT CTGGAAGCA TCTCTACATG TCACTTTAGG

101 CCGAAATAT ACACATGACT GAAGGAAGG AGCTCGTCAT TCCCTGCCG GTTACGTCAC CTAACATCAC TGTACTTTA AAAAAGTTTC CACTTGACAC  
 GGCCTTAATA TGTGTACTGA CTTCTTCCC TCGAGCAGTA AGGACGGCC CAATGCAGTG GATTGTAGTG ACAATGAAAT TTTTTCAAAG GTGAACCTGTG

101 TTTGATCCCT GATGAAAAAC GCATAATCTG GGACAGTAGA AAGGCTTCA TCAATACAAA TGCAACGTAC AAAGAAATAG GGCTTCTGAC CTGTGAAGCA  
 AAAC TAGGGA CTACCTTTTG CGTATTAGAC CTTGTCTATCT TTCCCGAAGT AGTATAGTTT ACGTTGCATG TTTCTTTATC CCGAAGACTG GACACTTCGT

101 ACAGTCAATG GGCATTGTGA TAAGACAAAC TATCTCACAC ATCGACAAAC CAATACAATC  
 TGTCACTTAC CCGTAAACAT ATTCTGTTTG ATAGAGTGTG TAGCTGTTTG GTTATGTTAG

23/75

FIG. 25H

```

1 GAATTCAACT TCTCCATACT TTGGATAAGG AATATACAGAC ATGAAAATATC TCATTGCTGA GTTGTATTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT
CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGTCTG TACTTTTATAG AGTAACGACT CAACAATAAA TTCGAACGGG TTTTCTTCT TCTCAGCTTA

101 GAACCTGTGT CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACACGG GTTGATTGAT CAGGTAGAGG
CTTGACACAC GCGTCCATCT TCGAAACCTC TAATAGCAGT GACGTACGA AGCGTTATAC CGGTTTATAC TGGTTGTGCG CAACATACTA GTCCATCTCC

201 GGGCGTGTA CGAGGTAAAG CCCGATGCCA GCATTCTCTGA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA
CCCGCGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGAGG CGCTAATGCA TTTCTTCAAT AACTTCGTAG GACGAGTCAT

301 AAAAGTTAAT CTTTTCACAA GCTGTCAATA AGTTGTCACG GCCGAGACTT ATAGTCGGTT TGTTTTTTAT TTTTAATGTA TTTGTAACTA GTACGCAAGT
TTTTCAAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAAAATAA AAAATTACAT AAACATTGAT CATGCGTTCA

401 TCACGTAAA AGGGTATGTA GAGTTGAGG TGATTTTATG AAAAGAATA TCGCAATTCT TCTTGCATCT ATGTTCTGTT TTTCTATTGC TACAAATGCC
AGTGCATTTT TCCCATACAT CTCCAACCTC ACTAAATATC TTTTCTTAT AGCGTAAAGA AGAACGTAGA TACAAGCAAA AAAGATAACG ATGTTTACGG

1 M K K N I A F L L A S M F V F S I A T N A
^start of stII sequence

501 TATGCATCG ATATCCAGAT GACCCAGTCC CCGAGCTCCC TGTCGGCCTC TGTCGGCGAT AGGTCACCA TCACCTGCGG TGCCAGTCAG GATGTGTCCA
ATACGTAGGC TATAGGTCTA CTGGGTCAGG GGCTCGAGG ACAGCGGAG ACACCGCTA TCCCAGTGT AGTGGACGC ACGTCACTC CTACACAGGT

22 Y A S D I Q M T Q S P S L S A S V G D R V T I T C R A S Q D V S T
^light chain start

601 CTGCTGTAGC CTGCTATCAA CAGAAACCA GAAAGCTCC GAAGCTTCTG ATTTACTCGG CATCTTCTCT CTACTCTGGA GTCCCTTCTC GCTTCTCTGG
GACGACATCG GACCATAGTT GTCTTTGGTC CTTTTCGAGG CTTTCAAGAC TAAATGAGCC GTAGGAAGGA GATGACCT CAGGGAAGAG CGAAGAGACC

56 A V A W Y Q Q K P G K A P K L L I Y S A S F L Y S G V P S R F S G
^CDR-L2

701 TAGCGGTTCC GGGACGGATT TCACCTCGAC CATCAGCAGT CTGCAGCGG AAGACTTCG AACTTATATC TGTACGAAT CTTTACTAC TCCTCCACG
ATCGCCAAGG CCTGCTCTAA AGTGAGACTG GTAGTCGTCA GACGTCGGC TTCTGAAGC TTGAATAATG ACAGTCGTTA GAATATGATG AGGAGGTGC

89 S G S G T D F T L T I S S L Q P E D F A T Y Y C Q Q S Y T T P P T
^CDR-L3

```

FIG. 26A

1 TTCCGACAGG GTACCAAGGT GGAGATCAAA CGAAGTGTGG CTGCACCATC TGTCTTCATC TTCCCGCCAT CTGATGAGCA GTTGAATCT GGAAGTGCCT  
 AAGCTGTCC CATGGTTCCA CCTCTAGTTT GCTTGACACC GACGTGGTAG ACAGAAGTAG AAGGGCGTA GACTACTCGT CAACCTTAGA CCTTGACGGA  
 2 F G Q G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S  
 1 CTGTTGTGTG CCTGTGTAAT AACTTCTATC CCAGAGAGGC CAAAGTACAG TGAAGGTGG ATAACGCCCT CCAATCGGGT AACTCCCAGG AGAGTGTAC  
 GACAACACAC GGACGACTTA TTGAAGATAG GGTCTCTCCG GTTTCATGTC ACCTTCACC TATTGCGGA GGTAGCCCA TTGAGGTCC TCTCAGATG  
 6 V V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T  
 1 AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC ACCCTGACGC TGAGCAAGC AGACTACGAG AAACACAAAG TCTACGCCCTG CGAAGTCACC  
 TCTCGTCCCTG TCGTTCCTGT CGTGGATGTC GGAGTCGTG TGGACTGCG ACTCGTTTCG TCTGATGCTC TTTGTGTTTC AGATGCGGAC GCTTCAGTGG  
 9 E Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T  
 1 CATCAGGGCC TGAGCTCGCC CGTCACAAG AGCTTCAACA GGGGAGAGTG TGGTGCCAGC TCCGGATGG CTGATCCGAA CCGTTTCCGC GGTAAGGACC  
 GTAGTCCCGG ACTCGAGCGG GCAGTGTTC TCGAAGTTGT CCCCTCTCAC ACCACGGTGG AGGCATACC GACTAGGCTT GGCAAGGGC CCATTCCCTGG  
 2 H Q G L S S P V T K S F N R G E C G A S S G M A D P N R F R G K D L  
 ^end of light chain, start of gd tag  
 1 TGGCATAACT CGAGGCTGAT CCTCTACGCC GGACGCATCG TGGCCCTAGT AGCAAGTTC ACCTAAAAG GGTGAGGTG ATTTTATGAA  
 ACCGTATTGA GCTCCGACTA GGAGATGCGG CCTGCGTAGC ACCGGGATCA TCGGTTCAAG TGCATTTTTC CCATGATCT CCAACTCCAC TAAAATACTT  
 6 A O  
 3 M K  
 ^start of stII  
 1 AAAGAAATATC GCATTTCTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAACGGTA CGCTGAGGT CAGCTGGTGG AGTCTGGCGG TGGCCTGGTG  
 TTTCTTATAG CGTAAAGAAG AACGTAGATA CAAGCAAAA AGATAACGAT GTTTGGCAT GCGACTCAA GTCGACCACC TCAGACCGCC ACCGGACAC  
 1 K N I A F L L A S M F V F S I A T N A Y A E V Q L V E S G G L V  
 ^start of heavy chain  
 1 CAGCCAGGGG GCTCACTCCG TTTGTCTCTGT GCAGTCTCTG GCTTCAACAT TAAAGACACC TATATACACT GGGTGGCTCA GGGCCCCGGT AAGGCGCTGG  
 GTCGTCGCC CGAGTGAGGC AAACAGGACA CGTCAAGAC CGAAGTTGTA ATTTCTGTGG ATATATGTA CCCACGAGT CCGGGGCCCA TTCCCGGACC  
 3 Q P G G S L R L S C A A S G F N I K D T Y I H W V R Q A P G K G L E  
 ^CDR-H1

FIG. 26b

1501 AATGGGTTGC AAGGATTAT CCTACGAATG GTTATACTAG ATATGGCGAT AGCGTCAAGG GCGGTTTCAC TATAAGCGCA GACACATCCA AAAACACAGC  
 TTACCCAACG TTCCCTAAATA GGATGCTTAC CAATATGATC TATACGGCTA TCGCAGTTCC CGGCAAAAGT ATATTCCGGT CTGTGTAGGT TTTTGTGTGG  
 47 W V A R I Y P T N G Y T R Y A D S V K G R F T I S A D T S K N T A  
 ^CDR-H2  
 1601 CTACCTACAA ATGAACAGCT TAAGAGCTGA GGACACTGCC GTCTATTATT GTAGCCGCTG GGGAGGGGAC GGCTTCTATG CTATGGACTA CTGGGGTCAA  
 GATGGATGTT TACTTGTGCA ATTCTCGACT CCTGTGACGG CAGATAATAA CATCGGGGAC CCCTCCCTCG CCGAAGATAC GATACCTGAT GACCCCAAGTT  
 80 Y L Q M N S L R A E D T A V Y Y C S R W G G D G F Y A M D Y W G Q  
 ^CDR-H3  
 1701 GGAACACTAG TCACCGTCTC CTCGGCCCTCC ACCAAGGGCC CATCGGTCTT CCCCCTGGCA CCTCTCTCCA AGAGCACCTC TGGGGGCACA GCGGCCCTGG  
 CCTTGTGATC AGTGGCAGAG GAGCCGGAGG TGGTTCCCGG GTAGCCAGAA GGGGACCGT GGGAGGAGGT TCTCTGTGAG ACCCCCGTGT CGCCGGGACC  
 113 G T L V T V S S A S T K G P S V F P L A P S S K S T S G G T A A L G  
 1801 GCTGCCTGGT CAAGGACTAC TTCCCCGAAC CGGTGACGCT GTCGTGAAC TCAGGGGCCC TGACACACGG CGTGACACCC TTCCCGGCTG TCCTACAGTC  
 CGACGGACCA GTTCTGTATG AAGGGGCTTG GCCACTGCCA CAGCACCTTG AGTCCGCGGG ACTGCTGCCC GCACGTGTGG AAGGGCCGAC AGGATGTGAG  
 147 C L V K D Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S  
 1901 CTCAGGACTC TACTCCCTCA GCAGCGTGGT GACCGTGCCC TCCAGCAGCT TGGGCACCCA GACCTACATC TGCAACGTGA ATCACAAGCC CAGCAACACC  
 GAGTCCTGAG ATGAGGGAGT CGTGCACACA CTGGCACGGG AGGTGCTCGA ACCCGTGGGT CTGGATGTAG ACGTTGCACT TAGTGTTCGG GTCGTTGTGG  
 180 S G L Y S L S S V V T V P S S S L G T Q T Y I C N V N H K P S N T  
 2001 AAGGTCGACA AGAAAGTTGA GCCCAATCT TGTGACAAA CTCACGGCGG CATGAACAG CTAGAGGACA AGGTGGAAGA GCTACTCTCC AAGAACTACC  
 TTCCAGCTGT TCTTTCACT CGGGTTTAGA ACACGTGTTT GAGTGCCGGC GTACTTTGTC GATCTCCTGT TCCAGCTTCT CGATGAGAGG TTCTTTGATGG  
 213 K V D K K V E P K S C D K T H G R M K Q L E D K V E E L L S K N Y H  
 ^end of heavy chain, start of leucine zipper  
 2101 ACCTAGAGAA TGAAGTGGCA AGACTCAAAA AACTTGTGCG GGAGCGCGGA AAGCTTAGTG GCGGTGGCTC TGGTTCCGGT GATTGTGATT ATGAAGAAGAT  
 TGGATCTCTT ACTTCACCGT TCTGAGTTT TTGAACAGCC CCTCGGCGCT TTGCAATCAC CGCCACCGAG ACCAAGGCCA CTAATACTAA TACTTTTCTA  
 247 L E N E V A R L K K L V G E R G K L S G G G S G S G D F D Y E K M  
 end of leucine zipper, start of gene III coat protein (267-end)^

FIG. 26C

2201 GGCAACCGCT AATAAGGGG CTATGACCGA AAATGCCGAT GAACACGGC TACAGTCTGA CGCTAAAGGC AAATTTGATT CTGTGCGTAC TGATTACGGT  
 CCGTTTGGCA TTATTCCCC GATACCTGGCT TTTACGGCTA CTTTTCGGCG ATGTCAGACT GCGATTTCG TTTGAACATA GACAGCGATG ACTAATGCCA  
 280 A N A N K G A M T E N A D E N A L Q S D A K G K L D S V A T D Y G  
 2301 GCTGCTATCG ATGGTTTCAT TGGTGACGTT TCCGGCCCTG CTAATGGTAA TGGTGCTACT GGTGATTTTG CTGGCTCTAA TTCCCAAAATG GCTCAAGTCG  
 CGACGATAGC TACCAAAAGTA ACCACTGCAA AGCCCGGAAC GATTACCATT ACCACGATGA CCACATAAAC GACCGAGATT AAGGTTTAC CGAGTTCAGC  
 313 A A I D G F I G D V S G L A N G N G A T G D F A G S N S Q M A Q V G  
 2401 GTGACGGTGA TAATTCACCT TTAATGAATA ATTTCCGTCA ATATTACCT TCCCTCCCTC AATCGGTGA ATGTCGCCCT TTTGTCTTTA GCGCTGGTAA  
 CACTGCCACT ATTAAGTGA AATTACTTAT TAAAGGCAGT TATAATGGA AGGAGGGAG TTAGCCAAT TACAGCGGGA AACAGAAAT CCGACCAATT  
 347 D G D N S P L M N N F R Q Y L P S L P Q S V E C R P F V F S A G K  
 2501 ACCATATGAA TTTTCTATTG ATTGTGACAA AATAAACATA TTCCGTGGTG TCTTTTCGTT TCTTTTATAT GTTGCCACCT TTATGTTATGT ATTTTCTACG  
 TGGTATACCT AAAAGATAAC TAACACTGTT TTATTTGAAT AAGGCACCAC AGAAACGCAA AGAAATATA CAACGGTGA AATACATACA TAAAAGATGC  
 380 P Y E F S I D C D K I N L F R G V F A F L L Y V A T F M Y V F S T  
 2601 TTTGCTAACA TACTGCGTAA TAAGGACTCT TAATCATGCC AGTTCTTTTG GCTAGCGCG CCGTATACCT TGCTGCGCTC CCGCGCTGTC GTGCGGGTGC  
 AAACGATTGT ATGACGCATT ATTCTCTAGA ATTAGTACGG TCAAGAAAC CCAATCGCGG GGAATATGGA ACAGACGGAG GGGCGCAACG CAGCGCCACG  
 413 F A N I L R N K E S O  
 2701 ATGGAGCCGG GCCACCTCGA CCTGAATGGA AGCCGGCGGC ACCTCGCTAA CCGATTACCC ACTCCAAGAA TTGGAGCCAA TCAATTCTTG CGGAGAATCG  
 TACCTCGGCC CCGTGGAGCT GGACTTACCT TCGGCCCGCG TGGAGCGATT GCTAAGTGG TGAGGTTCTT AACCTCGGTT AGTTAAGAAC GCCTCTTGAC  
 2801 TGAATGCGCA AACCAACCCT TGGCAGACA TATCCATCGC GTCCGCCATC TCCAGCAGCC GCACCGGGC CATCTCGGC AGCGTTGGGT CCTGGGCCACG  
 ACTTACGCGT TTGGTTGGGA ACCGTCTGT ATAGGTAGCG CAGCGGTAG AGGTGTCGG CGTGGCGCG GTAGAGCCG TCGCAACCCA GGACCGGTGC  
 2901 GGTGCGCATG ATCGTGCTCC TGTCGTGAG GACCCGGCTA GGCTGGCGG GTTGCCCTTAC TGCTTAGCAG AATGAATCAC CGATACCGA CGGAACGTGA  
 CCACGCGTAC TAGCAGGAG ACAGCAACTC CTGGGCCGAT CCGACCGCCC CAACGGAATG ACCAATCGTC TTACTTAGTG GCTATGCGCT CGCTTGCACT  
 3001 AGCGACTGCT GCTGCAAAAC GTCGCGACC TGAGCAACAA CATGAATGCT CTTGCGTTTC CCGTTTTCGT AAAGTCTGGA AACCGGGAAG TCAGCGCCCT  
 TCGCTGACGA CGACGTTTTC CAGACGCTTG ACTCGTTGTT GTACTTACCA GAAGCCAAAG GCACAAAGCA TTTTCAGACCT TTGCGGCTTC AGTCGCGGGA

FIG. 26D



3101 GCACCATAT GTTCCGGATC TGCATCGGAG GATGCTGCTG GCTACCCCTGT GGAACACCTA CATCTGTATT AACGAGCGC TGGCATGAC CCTGAGTGAT  
 CGTGGTAATA CAAGGCCCTAG ACGTAGGCTC CTACGACGAC CGATGGACA CCTGTGGAT GTAGACATAA TTGCTTCGG ACCGTAAC TG GACTCACTA  
 3201 TTTTCTCTCG TCCCGCCGCA TCCATACCGC CAGTTGTTTA CCTCACAAC GTTCCAGTAA CCGGSCATGT TCATCATCAG TAACCCGTAAT CGTGAGCATC  
 AAAAGAGACC AGGCGGCGT AGGTATGGC GTCAACAAT GGGAGTGTG CAAGTCAAT GGCCTGTACA AGTAGTAGTC ATTGGGCATA GCATCTGTAG  
 3301 CTCTCTCTCT TCAATCGGTAT CATTACCCCC ATGAACAGAA ATTCCCCCTT ACACGGAGC ATCAAGTGAC CAAACAGGAA AAAACCCGCC TTAACATGGC  
 GAGAGAGCAA AGTAGCCATA GTAATGGGG TACTTGTCTT TAAGGGGAA TGTCCCTCCG TAGTTCAC TGTTGTCTT TTTTGGCGG AATTGTACCG  
 3401 CCGCTTTATC AGAAGCCAGA CATTAACGCT TCTGGAGAAA CTCAACGAGC TGGACGCGGA TGAACAGGCA GACATCTGTG AATCGCTTCA CGACCACGCT  
 GCGCAATAG TCTTCGGTCT GTAATTGCGA AGACCTCTTT GAGTTGCTCG ACCTGGCCT ACTTGTCCGT CTGTAGACAC TTAGCGAAGT GCTGTGCGA  
 3501 GATGAGCTTT ACCGCAGGAT CCGGAAATG TAAACGTTAA TATTTTCTTA AAATTCGCGT TAAATTTTG TTAATCAGC TCATTTTATA ACCAATAGGC  
 CTAATCGAAA TGGCGTCTTA GGCCTTTAAC ATTTGCAATT ATAAACAAT TTAAAGCGCA ATTAAAGC AATTAGTCG AGTAAAAAT TGGTTATCCG  
 3601 CGAAATCGC AAAATCCCTT ATAAATCAA AGAATAGACC GAGATAGGT TGAGTGTGT TCCAGTTTGG AACAAAGAGT CACTATATAA GAACGTGGAC  
 GCTTAGCCG TTTTAGGGAA TATTAGTTT TCTTATCTGG CTCTATCCCA ACTCACACA AGTCAAAACC TTGTTCTCAG GTGATAATTT CTGACACCTG  
 3701 TCCAACGTCA AAGGGGAAA AACCGTCTAT CAGGGCTATG GCCCACTAG TGAACCATCA CCTAATCAA GTTTTITGG GTGAGGTGC CGTAAAGCAC  
 AGGTGCGAGT TTCCCGCTTT TTGGCAGATA GTCCCGATAC CGGTGATGC ACTTGTGTAGT GGGATTAGT CAAAAAACCC CAGCTCCACG GCATTTCTGTG  
 3801 TAAATCGGA CCTAAAGGG AGCCCCCGAT TTAGAGCTTG ACGGGGAAAG CCGGCGAAG TGGCGAGAAA GGAAGGGAAG AAAGCGAAG GAGCGGGCGC  
 ATTTAGCCTT GGGATTCCC TCGGGGCTA AATCTCGAAC TGCCCCCTTC GCGCGTTC ACCGCTCTTT CCTTCCCTTC TTTCCCTTC CTGCCCCCGC  
 3901 TAGGGCGCTG GCAAGTGTAG CCGTCACGCT GCGCGTAACC ACCACACCG CCGCGCTTAA TGGCGCGCTA CAGGGCGCT CCGGATCCTG CCTCGCGCTG  
 ATCCCGCGAC CATTACATC GCCAGTGGC CCGCATTTGG TGGTGTGGG GCGCGGAATT ACGCGCGAT GTCCCGCGCA GGCCTAGGAC GGAGCGCGCA  
 4001 TTCGGTGATG ACGGTGAAA CCTCTGACAC ATGACGCTCC CCGAGACGCT CAGAGACGCT CTGTAAGCGG ATGCCGGGAG CAGACAAAGC CGTCAGGGCG  
 AAGCCACTAC TGCCACTTTT GGAGACTGTG TAGGTGCGAG GCCTCTGCCA GTGTGGAACA GACATTCGCC TACGGCCCTC GTCTGTTCGG GCAGTCCCGC  
 4101 CGTCAGCGG TGTGGCGGG GTTCGGGGG CAGCCATGAC CCAGTCACGT ACCGATAGCG GAGTGTATAC TGGCTAACT ATCGGCGATC AGAGCAGATT  
 GCAGTCGCC ACAACGGCC ACAGCCCCG GTCGGTACTG GGTGAGTGA TCGCTATCG CTCACATATG ACCGAATGA TACGGCGTAG TCTCGTCTAA

FIG. 24 E



4201 GTACTGAGAG TGCACCATAT GCGGTGTGAA ATACCGCACA GATCGGTAAG GAGAAAATAC CGCATCAGGC GCTCTTCCGC TTCTCTCGCTC ACTGACTCGC  
 CATGACTCTC ACGTGGTATA CGCCACACTT TATGGCGTGT CTACGCATTC CTCCTTTATG GCGTAGTCCG CGAGAAGGG AAGGAGCGAG TGACTGAGCG  
  
 4301 TCGGCTCGGT CGTTGGGCTG CCGCGAGCGG TATCAGCTCA CTCAAAGCG GTAATACGGT TATCCACAGA ATCAGGGGAT AACGCAGGAA AGAACATGTG  
 ACGGAGCCCA GCAAGCCGAC GCGGCTCGCC ATAGTCGAGT GAGTTTCCGC CATATGCCA ATAGGTCT TAGTCCCTA TTGCGTCCCTT TCTTGTACAC  
  
 4401 AGCAAAAGGC CAGCAAAAGG CCAGGAACCG TAAAAGGCC GCGTTGCTGG CGTTTTCCTA TAGGTCCTGC CCCCCTGACG AGCATCAAA AAATCGACGC  
 TCGTTTTCGG GTCCCTTCC GGTCTTTCCG ATTTTTCGG CGCAACGACC GCAAAAAGGT ATCCGAGGCG GGGGACTGC TCGTAGTCTT TTTAGCTGCG  
  
 4501 TCAAGTCAGA GGTGGCGAAA CCCGACAGGA CTATAAAGAT ACCAGGCGTT TCCCCCTGGA AGTCCCTCCG TCGGCTCTCC TGTTCCGACC CTGCCGCTTA  
 AGTTCAGTCT CCACCGCTTT GGGCTGTCTT GATATTTCTA TGGTCCGCAA AGGGGACCT TCGAGGGAGC ACGGAGAGG ACAAGGCTGG GACGGCGAAT  
  
 4601 CCGGATACCT GTCCGCCCTT CTCCCTTCGG GAAGCGTGGC GCTTCTCTAT AGCTCAGCT GTAGGTATCT CAGTTCGGTG TAGTTCGTTT GCTCCAAAGCT  
 GGCCTATGGA CAGGCGGAAA GAGGGAAGCC CTTCGACCG CGAAGAGTA TCGAGTCCGA CATCCATAGA GTCAAGCCAC ATCCAGCAAG CGAGGTTCGA  
  
 4701 GGGCTGTGTG CACGAACCCC CCGTTCAGCC CGACCGGTGC GCCTTATCCG GTAACATATCG TCTTGAGTCC AACCCGGTAA GACAGGACTT ATCGCCACTG  
 CCCGACACAC GTGCTTGGG GGCAGTCCG GCTGGCCAG CGGAATAGC CATGTATAGC AGAATCAGG TTGGGCCATT CTGTGCTGAA TAGCGGTGAC  
  
 4801 GCAGCAGCCA CTGGTAACAG GATTAGCAGA GCGAGGTATG TAGGCGGTGC TACAGAGTTC TTGAAGTGGT GGCCTAACHA CGGCTACACT AGAAGGACAG  
 CGTCGTCCGT GACCATTGTC CTAATCGTCT CGCTCCATAC ATCCGCCAG ATGTCTCAAG AACTTCACCA CCGGATTGAT GCGGATGTA TCTTCTCTGTC  
  
 4901 TATTTGGTAT CTGGGCTCTG CTGAAGCCAG TTACTTTCGG AAAAAGAGTT GGTAGTCTTT GATCCGGCAA ACAAAACCACC GCTGGTAGCG GTGGTTTTTT  
 ATAAACCATA GACGCGAGAC GACTTCGGTC AATGGAAGCC TTTTCTCTCA CCATCGAGAA CTAGGCCGTT TGTTTGGTGG CGACCATCGC CACCAGAAAA  
  
 5001 TGTTTGCAAG CAGCAGATTA CCGCAGAAA AAAAGGATCT CAAGAAGATC CTTTGAATCT TTCTACGGG TCTGACGCTC AGTGAACGA AAATCAGCT  
 ACAACGTTT GTCGTCTAAT GCGGCTCTTT TTTTCTCTAGA GTTCTCTTAG GAAACTAGAA AAGATGCCCC AGACTGCGAG TCACCTTGGT TTTGAGTGCA  
  
 5101 TAAGGGATTT TGGTCATGAG ATTATCAAAA AGGATCTTCA CCTAGATCCT TTTAAATTAA AAATGAAGTT TTAAATCAAT CTAAAGTATA TATGAGTAAA  
 ATCCCTAAA ACCAGTACT TAATAGTTTT TCCTAGAAGT GGATCTAGGA AAATTTAATT TTTACTTCAA AATTTAGTTA GATTTCATAT ATACTCATTT  
  
 5201 CTTGGTCTGA CAGTTACCAA TGCTTAATCA GTGAGGCACC TATCTCAGCG ATCTCTCTAT TTCTGTTTATC CATAGTTGCC TGACTCCCCG TCGTGTAGAT  
 GAACCAAGCT GTCAATGGTT ACGAATTAGT CACTCCGTGG ATAGAGTCG TAGACAGATA AAGCAAGTAG GTATCAACGG ACTGAGGGG AGCACATCTA

FIG. 26f

5301 AACTACGATA CGGAGGGCT TACCATCTGG CCCAGTCTG GCAATGATAC CGCAGAGACC AGCTCACCG GCTCCAGATT TATCAGCAAT AAACAGCCA  
 TTGATGCTAT GCCCTCCGA ATGGTAGACC GGGGTACGA CGTTACTATG GCGCTCTGG TCGAGTGGC CGAGTCTAA ATAGTCGTTA TTTGGTGGT  
  
 5401 GCCGGAAGG CCGAGCGCAG AAGTGGTCTT GCAACTTTAT CCGCCTCCAT CCAGTCTATT AATGTTGCC GGAAGCTAG AGTAAGTAGT TCGCCAGTTA  
 CGGCCCTCCC GGCTCGGCTC TTCACCAGGA CGTTGAAATA GCGGAGGTA GGTCAATAA TTAACAACGG CCCTTCGATC TCATTCATCA AGCGTCAAT  
  
 5501 ATAGTTGGC CAACGTTGTT GCCATGTCTG CAGGATCTGT GGTGTACGC TCGTCTGTTG GTATGGCTTC ATTCAGCTCC GGTCCCAAC GATCAAGGCG  
 TATCAAACGC GTTGCAACAA CCGTAACGAC GTCCGTAGCA CCACAGTGGC AGCAGCAAC CATAACGAAG TAAGTCGAGG CCAAGGGTTG CTAGTCCCGC  
  
 5601 AGTTACATGA TCCCCCATGT TGTGCAAAA AGGGTTAGC TCCTTCGGTC CTCCGATCGT TGTCAAGAAGT AAGTTGGCG CAGTGTATC ACTCATGGTT  
 TCAATGTACT AGGGGGTACA ACACGTTTTT TCGCCAATCG AGGAAGCCAG GAGGCTAGCA ACAGTCTTCA TTCAACCCGC GTCACAATAG TGAGTACCAA  
  
 5701 ATGGCAGCAC TGCATAATTC TCTTACTGTC ATGCCATCCG TAAGATGCTT TTCTGTGACT GGTGAGTACT CAACCAAGTC ATTCTGAGAA TAGTGTATGC  
 TACCCTCGTG ACGTATTAG AGAATGACAG TACGCTAGGC ATTCTACGAA AAGACACTGA CCACTCATGA GTTGGTTCAG TAAGACTCTT ATCACATACG  
  
 5801 GCGACCGAG TTGCTCTTGC CCGCGCTCAA CACGGGATAA TACCGGCCA CATAGCAGAA CTTTAAAGT GCTCATCATT GGAAAACGTT CTTCGGGGCG  
 CCGTGGCTC AACGAGACG GGCCGCGATT GTGCCCTATT ATGGCGGGT GTATCGTCTT GAAATTTTCA CGAGTAGTAA CCTTTTGCAA GAAGCCCCG  
  
 5901 AAAACTCTCA AGGATCTTAC CGCTGTTGAG ATCCAGTTCC ATGTAACCCA CTCGTGCACC CAACTGATCT TCAGCATCTT TTACTTTTAC CAGCGTTTCT  
 TTTTGAGAGT TCCTAGATG CCGACAATC TAGGTCAAGC TACATGGGT GAGCACGTGG GTTGACTAGA AGTCGTAGAA AATGAAAAGT GTCGCAAGA  
  
 6001 GGGTGAGCAA AAACAGGAAG GCAAAATGCC GCAAAAGG GATAAGGGC GACACGGAAA TGTGATATAC TCATCTCTT CCTTTTTC AA TATTATTGAA  
 CCCACTCGTT TTTGTCTTTC CGTTTACGG CGTTTTCCTT CCTATTTCCT CTGTGCTTTC ACAACTATG AGTATGAGAA GGAAAAGTT ATAATAACTT  
  
 6101 GCATTATCA GGGTTATTGT CTCATGAGCG GATACATATT TGAATGTATT TAGAAAAATA AACAAATAGG GGTTCGGCG ACATTTCCCG GAAAAGTGCC  
 CGTAAATAGT CCAATAACA GAGTACTCCG CTATGTATAA ACTTACATAA ATCTTTTTAT TTGTTTATCC CCAAGGGCGG TGTAAGGGG CTTTTTCACG  
  
 6201 ACCTGACGTC TAAGAAACCA TTATTATCAT GACATTAAAC TATAAAAATA GGCATATCAC GAGGCCCTTT CGTCTTCAAT ACAGGTAGAC CTTTCGTAGA  
 TGGACTGCAG ATTCTTTGGT AATAATAGTA CTGTAATTGG ATATTTTTAT CCGCATAGTG CTCGGGAAA GCAGAAAGTA TGTCCATCTG GAAAGCATCT  
  
 6301 GATGTACAGT GAAATCCCG AAATTATACA CATGACTGAA GGAAGGGAGC TCGTCATTC CCGCGGGT ACGTCACCTA ACATCACTGT TACTTTAAAA  
 CTACATGTCA CTTTAGGGC TTTAATATGT GTACTGACTT CCTTCCCTCG AGCAGTAAG GACGGCCAA TGCAGTGGAT TGTAGTGACA ATGAAATTTT

FIG. 26

6401 AAGTTTCCAC TTGACACTTT GATCCCTGAT GGAAAACGCA TAATCTGGGA CAGTAGAAG GGTTCATCA TATCAAAATGC AACGTACAAA GAAATAGGGC  
 TTCAAAGGTG AACTGTGAAA CTAGGGACTA CCTTTTGGGT ATTAGACCCT GTCACTCTTC CCGAAGTAGT ATAGTTTACG TTGCATGTTT CTTTATATCCCG  
  
 6501 TTCTGACCTG TGAAGCAACA GTCAATGGGC ATTTGTATAA GACAAACTAT CTCACACATC GACAAACCAA TACAATACAG GTAGACCTTT CGTAGAGATG  
 AAGACTGGAC ACTTCGTGT CAGTTACCCG TAAACATATT CTGTTTGATA GAGTGTGAG CTGTTTGGGT ATGTTATGTC CATCTGGAAA GCATCTCTAC  
  
 6601 TACAGTGAAA TCCCCGAAAT TATACACATG ACTGAAGGAA GGGAGCTCGT CATTCCTGTC CGGGTTACGT CACCTAACAT CACTGTTACT TTAAAAAAGT  
 ATGTCACCTT AGGGGCTTTA ATATGTGTAC TGACTTCCTT CCTCGAGCA GTAAGGAGC GCCCAATGCA GTGGATTGTA GTGACAAATGA AATTTTTC  
  
 6701 TTCCACTTGA CACTTTGATC CCTGATGGAA AACGCATAAT CTGGGACAGT AGAAGGGCT TCATCATATC AAATGCAACG TACAAAGAAA TAGGGCTTCT  
 AAGGTGAAC GTGAAACTAG GGAATACCTT TTGCGTATTA GACCTGTCA TCCTTCCCGA AGTAGATAG TTTACGTTGC ATGTTTCTTT ATCCCGAAGA  
  
 6801 GACCTGTGAA GCAACAGTCA ATGGGGCAATTT GTATAAGACA AACTATCTCA CACATCGACA AACCAATACA ATCTACAGGT AGACCTTTTC TAGAGATGTA  
 CTGGACACTT CGTTGTGAGT TACCCGTAAA CATATTCTGT TTGATAGAGT GTGTAGCTGT TTGGTTATGT TAGATGTCCA TCTGGAAAGC ATCTCTACAT  
  
 6901 CAGTGAAATC CCCGAAATTA TACACATGAC TGAAGGAAGG GAGCTCGTCA TTCCCTGCCG GGTACGTCA CCTAACATCA CTGTTACTTT AAAAAAGTTT  
 GTCACCTTTAG GGGCTTTAAT ATGTGTACTG ACTTCCCTCC CTCGAGCAGT AAGGACGGC CCAATGCCAGT GGATGTAGT GACAAATGAAA TTTTTCATAA  
  
 7001 CCACTTGACA CTTTGATCCC TGATGGAAAA CGCATAATCT GGGACAGTAG AAAGGGCTTC ATCATATCAA ATGCAACGTA CAAAGAAATA GGGCTTCTGA  
 GGTGAACGTG GAAACTAGGG ACTACCTTTT GCGTATTAGA CCTGTCTATC TTTCCCGAAG TAGTATAGTT TACGTGTCAT GTTTCCTTTAT CCCGAAGACT  
  
 7101 CCTGTGAAGC AACAGTCAAT GGGCATTGTG ATAAAGACAAA CTATCTCACA CATCGACAAA CCAATACAAT C  
 GGACACTTCG TTGTCAGTTA CCCGTAAACA TATTCTGTTT GATAGAGTGT GTAGCTGTTT GGTATGTGA G

FIG. 24 H

```

1 ATGAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTG TTTTCTTAT TGCACAAAT GCCTATGCAG ATATCCAGAT GACCCAGTCC CCGAGCTCCC
TACTTTTCT TATAGGCTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTA CCGATACGTC TATAGGTCTA CTGGGTCAGG GGCTCGAGGG
1M K K N I A F L L A S M F V F S I A T N A Y A D I Q M T Q S P S S L
^met
^start of stII signal sequence
^start of light chain

101 TGTCCGCCTC TGTGGCGGAT AGGGTCACCA TCACCTGCCG TGCAGTCAG GATGTGTCCA CTGCTGTAGC CTGGTATCAA CAGAAACCAG GAAAAGCTCC
ACAGGCGGAG ACACCGGCTA TCCCAGTGGT AGTGGACGGC ACGETCAGTC CTACACAGGT GACGACATCG GACCATAGTT GTCTTTGGTC CTTTTCGAGG
35 S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K P G K A P
^CDR-L1

201 GAAGCTTCTG ATTACTCGG CATCCTTTCT CTACTCTGGA GTCCCTTCTC GCTTCTCTGG TAGCGGTTC GGGACGGATT TCACCTCTGAC CATCAGCAGT
CTTCGAAGAC TAAATGAGCC GTAGGAAGG GATGAGACCT CAGGGAAGAG CGAAGAGACC ATCGCCAAGG CCCTGCCCTAA AGTGAGACTG GTAGTCGTCA
68 K L L I Y S A S F L Y S G V P S R F S G S G S G T D F T L T I S S
^CDR-L2

301 CTGCAGCCGG AAGACTTCGC AACTTATTAC TGTACGAAC ATTATACTAC TCCTCCACG TTTCGGACAGG GTACCAAGGT GGAGATCAA CGAACTGTGG
GACGTCGGCC TTCTGAAGCG TTGAATAATG ACAGTCGTTG TAATATGATG AGGAGGGTGC AAGCCTGTCC CATGTTGCCA CCTCTAGTTT GCTTGACACC
101 L Q P E D F A T Y Y C Q Q H Y T T P P T F G Q G T K V E I K R T V A
^CDR-L3

401 CTGCACCATC TGTCTTCATC TTCCCGCCAT CTGATGAGCA GTTGAATCT GGAACCTGCT CTGTTGTGTG CCTGCTGAAT AACITCTATC CCAGAGAGGC
GACGTGGTAG ACAGAAAGTAG AAGGGCGGTA GACTACTCGT CAACTTTAGA CTTTGACGGA GACACACAC GGACGACTTA TTGAAGATAG GGTCTCTCCG
135 A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E A

501 CAAAGTACAG TGAAGGTGG ATAACGCCCT CCAATCGGGT AACTCCCAGG AGAGTGTAC AGACCAAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC
GTTTCATGTC ACCTTCCACC TATTGCGGGA GGTAGGCCA TTGAGGGTCC TCTCACAGTG TCTGCTCTCTG TCGTTCTCTG CGTGGATGTC GGAGTCGTCG
168 K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S S

601 ACCCTGACG TGAGCAAAGC AGACTACGAG AAACACAAG TCTACGCCCT GAAAGTCACC CATCAGGGCC TGAGTCGCC CGTCACAAAG AGCTTCACAA
TGGGACTGCG ACTCGTTTCG TCTGATGCTC TTTGTGTTTC AGATGGGAC GCTTCAGTGG GTAGTCCCGG ACTCAGCGG GCAGTGTTC TCGAAGTTGT
201 T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N R

```

FIG. 27A

701 GGGGAGAGTG TGGTGCCAGC TCCGGGTATGG CTGATCCGAA CCGTTTCCGC GGTAAAGGACC TGGCATAACT CGAGGCTGAT CCTCTACGCC GGACGCATCG  
 CCCCTCTCAC ACCACGGTGG AGGCCATACC GACTAGGCTT GGCAAAGGCG CCATTCCTGG ACCGTATTGA GCTCCGACTA GGAGATGCGG CCTGCGGTAGC  
 235 G E C G A S S G M A D P N R F R G K D L A O  
 ^end of light chain, start of gd tag  
  
 801 TGGCCCTAGT ACACAAGTTC ACCTAAAAG GGTAACTAGA GGTGAGGTG ATTTTATGAA AAAGAATATC GCATTTCTTC TTGCATCTAT GTTCGTTTTT  
 ACCGGGATCA TCGGTTCAAG TGCATTTTTC CCATTGATCT CCAACTCCAC TAAATACTTT TTTCCTATAG CGTAAAGAAG AACGTAGATA CAAGCAAAAA  
 -23 M K K N I A F L L A S M F V F  
 ^start of stII  
  
 901 TCTATTGCTA CAAACGCGTA CGCTGAGGTT CAGCTGGTGG AGTCTGGCGG TGGCCTGGTG CAGCCAGGGG GCTCACTCCG TTGTGCTCTGT GCAGCTTCTG  
 AGATAACGAT GTTTGGCGAT GCGACTCCAA GTCGACCCACC TCAGACCCGC ACCGGTCCCG GTCGGTCCCG CGAGTGAGGC AAACAGGACA CGTCGAAGAC  
 -8 S I A T N A Y A E V Q L V E S G G G L V Q P G G S L R L S C A A S G  
 ^start of heavy chain  
 ^CDR-H1  
  
 001 GCTTACCAT TAGTGGTTCT TGGATACACT GGGTGCGTCA GGGCCCGGCT AAGGGCCTGG AATGGGTTCG TTGGATTGCT CCTTATAGCG GCGCTACTGA  
 CGAAGTGCTA ATCACCAGA ACCTATGTGA CCCACGCGAT CCGGGGCCCC TTCCCGGACC TTACCCCAAG AACCTAACGA GGAATATCGC CGCGATGACT  
 27 F T I S G S W I H W V R Q A P G K G L E W V A W I A P Y S G A T D  
 ^CDR-H2  
  
 101 CTATGCCGAT AGCGTCAAGG GCGGTTTCAC TATAAGGCA GACACATCA AAAACACAGC CTACCTACAA ATGAACAGCT TAAGAGCTGA GGACACTGCC  
 GATACGGCTA TCGCAGTTC CCGCAAAGTG ATATTGCGGT CTGTGCTAGT TTTTGTGTGG GATGGATGTT TACTTGTCTGA ATTCTCGACT CCTGTGACGG  
 60 Y A D S V K G R F T I S A D T S K N T A Y L Q M N S L R A E D T A  
  
 201 GTCTATTATT GTGCAAGAGA GGGGGGCTTG TACTGGGTGT TCGACTACTG GGGTCAAGGA ACACCTAGTCA CCGTCTCTCT GGCCTCCACC AAGGGCCCAT  
 CAGATAATAA CACGTTCTCT CCCCCCGAAC ATGACCCACA AGCTGATGAC CCCAGTTTCT TGTGATCAGT GGCAGAGGAG CCGGAGGTGG TTCCCGGGTA  
 93 V Y Y C A R E G G L Y W V F D Y W G Q G T L V T V S S A S T K G P S  
 ^CDR-H3  
  
 301 CGGTCTTTCC CCTGGCACC TCCTCCAAGA GCACCTCTGG GGGCACAGCG GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGGTGC  
 GCCAGAAGGG GGACCGTGG AGGAGGTTCT CGTGGAGACC CCGGTCTGCG CCGGACCCGA CGGACCAAGT CCTGATGAG GGGCTTGGCC ACTGCCACAG  
 127 V F P L A P S S K S T S G G T A A L G C L V K D Y F P E P V T V S

FIG. 27B

1401 GTGGAACCTCA GCGGCCCTCTGA CCAGCGGGCGT GCACACCTTC CCGGCTGTCC TACAGTCTCTC AGGACTCTAC TCCCTCAGCA GGTGGTGAC CGTGCCTCTCC  
 CACCTTGAGT CCGCGGGACT GGTCCCGCA CCGTGTGAAG GCGCGACAGG ATGTGAGAG TCCTGAGATG AGGGAGTCGT CGCACCACTG GCACGGGAGG  
 160 W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V T V P S  
 1501 AGCAGCTTGG GCACCCAGAC CTACATCTGC AACGTGAATC ACAGCCAG ACACACCAAG GTCGACAAGA AAGTTGAGCC CAAATCTTGT GACAAAACTC  
 TCGTCGAACC CGTGGGCTG GATGTAGACG TTGCACCTAG TGTTGGGCTC GTTGTGGTTC CAGCTGTCTT TTCAACTCGG GTTTAGAACA CTGTTTGTAG  
 193 S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S C D K T H  
 1601 ACCTCAGTGG CCGTGGCTCT GGTCCGGTG ATTTTGATTA TGAAGAAGATG GCAAACGCTA ATAAGGGGCG TATGACCGAA AATGCCGATG AAAACGGCGT  
 TGGAGTCACC GCCACCGAGA CCAAGGCCAC TAAACTAAT ACTTTTCTAC CGTTGGGAT TATTCGCCG ATACTGGCTT TTACGGCTAC TTTTGGCGGA  
 227 L S G G S G S G D F D Y E K M A N A N K G A M T E N A D E N A L  
 ^end of heavy chain  
 ^start of gene III coat protein (267-end)  
 1701 ACAGTCTGAC GCTAAAGGCA AACTTGATTC TGTCGCTACT GATTACGGTG CTGTATCGA TGGTTTCATT GGTGACGTTT CCGGCCCTGC TAATGGTAAT  
 TGTGAGACTG CGATTTCGT TTGAACAAAG ACAGCGATGA CTAATGCCAC GACGATAGCT ACCAAAGTAA CCACGTGCAA GGCCGGAAAG ATTACCATTA  
 260 Q S D A K G K L D S V A T D Y G A A I D G F I G D V S G L A N G N  
 1801 GGTGCTACTG GTGATTTTGC TGGCTCTAAT TCCCAAATGG CTCAAGTCGG TGACGGTGAT AATTCACCTT TAATGAATAA TTTCCGTCAA TATTACCTT  
 CCACGATGAC CACTAAAACG ACCGAGATTA AGGGTTTACC GAGTTCAGCC ACTGCCACTA TTAAGTGGAA ATTACTTATT AAAGGCAGTT ATAAATGGAA  
 293 G A T G D F A G S N S Q M A Q V G D G D N S P L M N N F R Q Y L P S  
 1901 CCCTCCCTCA ATCGGTTGAA TGTGCGCCTT TTGTCTTTAG CGCTGGTAA CCATATGAAT TTTCTATTGA TTGTGACAAA ATAAACTTAT TCCGTGGTGT  
 GGGAGGGAGT TAGCCAACCT ACAGCGGGAA AACAGAAATC GCGACCATTT GGTATACTTA AAAGATAACT AACACTGTTT TATTGATA AGCACCAACA  
 327 L P Q S V E C R P F V F S A G K P Y E F S I D C D K I N L F R G V  
 2001 CTTTGGCTTT CTTTATATG TTGCCACCTT TATGTATGTA TTTTCTACGT TTGCTAACAT ACTCGGTAAT AAGGAGTCTT AA  
 GAAACGCCAA GAAATATAC AACGGTGGAA ATACATACAT AAAAGATGCA AACGATTGTA TGACGCATTA TTCTCAGAA TT  
 360 F A F L L Y V A T F M Y V F S T F A N I L R N K E S O

FIG. 27C

1 ATGAAAAGA ATATGGCAT TCTTCTTGCA TCTATGTTTCG TTTTTCTAT TGCTACAAAT GCCATATGCAG ATATCCAGAT GACCCAGTCC CCGAGCTCCC  
TACTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAGATA ACGATGTTTA CGGATACGTC TATAGGTCTA CTGGGTGAGG GGCTCGAGGG  
 1 M K K N I A F L L A S M F V F S I A T N A Y A D I Q M T Q S P S S L  
 ^met  
 ^start of stII signal sequence  
 ^start of light chain  
 101 TGTCGGCCTC TGTGGGCGAT AGGGTCACCA TCACCTGCCG TGCCAGTCAG GATGTGTCCA CTGCTGTAGC CTGSTATCAA CAGAAACCAG GAAAAGCTCC  
ACAGGGCGGAG ACACCCGCTA TCCCAGTGGT AGTGGACGGC ACGGTCAGTC CTACACAGGT GACGACATCG GACCATAGTT GTCTTTGGTC CTTTTCGAGG  
 35 S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K P G K A P  
 ^CDR-L1  
 201 GAAGCTTCTG ATTACTCGG CATCCTTCCT CTACTCTGGA GTCCCTTCTC GCTTCTCTGG TAGGGGTCC GGGAGGATT TCACTCTGAC CATCAGCAGT  
CTTCGAAGAC TAAATGAGCC GTAGGAAGGA GATGAGACCT CAGGGAAGAC CGAAGAGACC ATCGCCAAGG CCCTGCCTAA AGTGAGACTG GTAGTCGTCA  
 68 K L L I Y S A S F L Y S G V P S R F S G S G S G T D F T L T I S S  
 ^CDR-L2  
 301 CTGCAGCCGG AAGACTTCG CACTTATTAC TGTCAGCAAC ATTATACTAC TCCTCCACG TTCGGACAGG GTACCAAGGT GGAGATCAA CGAACTCTGG  
GACGTCGGCC TTCTGAAGCG TTGAATAATG ACAGTCCTTG TAATATGATG AGGAGGGTGC AAGCCTGTCC CATGGTTCCA CCTCTAGTTT GCTTGACACC  
 101 L Q P E D F A T Y Y C Q Q H Y T T P P T F G Q G T K V E I K R T V A  
 ^CDR-L3  
 401 CTGCACCATC TGCTTTCATC TTCCCGCCAT CTGATGACCA GTTGAAATCT GGAACCTGCT CTGTGTGTG CCTGCTGAAT AACTTCTATC CCAGAGAGGC  
GACGTGGTAG ACAGAAGTAG AAGGGCGGTA GACTACTCGT CAACTTTAGA CCTTGACGGA GACAACACAC GGACGACTTA TTGAAGATAG GGTCTCTCCG  
 135 A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E A  
 501 CAAAGTACAG TGGAAGGTGG ATAACGCCCT CCAATCGGCT AACTCCAGG AGAGTGTAC AGAGCAGGAC ACCAAGGACA GCACCTACAG CCTCAGCAGC  
GTTTCATGTC ACCTTCCACC TATTGCGGGA GGTTAGCCCA TTGAGGGTCC TCTCACAGTG TCTCGTCTCTG TCGTTCCCTGT CGTGGATGTC GGAGTCGTGG  
 168 K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S S  
 601 ACCGTGACGC TGAGCAAAGC AGACTACGAG AAACACAAAG TCTACGCGTG CGAAGTCACC CATCAGGGCC TGAGCTCGCC CGTCACAAAG AGCTTCAACA  
TGGGACTGCG ACTCGTTTCG TCTGATGCTC TTTGTGTTTC AGATCGGAC GCTTCAGTGG GTAGTCCCGG ACTCGAGCGG GCAGTGTTC TCAAGTGTGT  
 201 T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N R

FIG. 28A

```

701 GGGGAGAGTG TGGTGCCAGC TCCGGTATGG CTGATCCGAA CCGTTTCCGC GGTAAAGGACC TGGCATAAAT CGAGGCTGAT CCTCTACGCC GGACGCATCG
    CCCCTCTCAC ACCACGGTGG AGGCCATACC GACTAGGCTT GGCAAGGCG CCATTCTGG ACCGTATTGA GCTCCGACTA GGAGATGCGG CCTGCGTAGC
235 G E C G A S S G M A D P N R F R G K D L A O
    ^end of light chain, start of gd tag

801 TGGCCCTAGT ACGCAAGTTC ACGTAAAG GGTAACTAGA GGTGAGGTG ATTTTATGAA AAGAATATC GCATTCTTC TTGCACTAT GTTCGTTTTT
    ACCGGGATCA TCGGTTCAAG TGCATTTTTC CCATTGATCT CCAACTCCAC TAAAAACTT TTCTTTATAG CGTAAAGAAG AACGTAGATA CAAGCAAAA
-23      M K K N I A F L L A S M F V F
    ^start of stII

901 TCTATTGCTA CAAACGCGTA CGCTGAGGTT CAGCTGGTGG AGTCTGGCGG TGGCTGGTG GCTCACTCCG TTTGTCTGT GCAGCTTCTG
    AGATAACGAT GTTTGGCAT GCGACTCCAA GTCGACCACC TCAGACCGCC ACCGGACCAC GTCCGTCCCC CGAGTGAGGC AAACAGGACA CGTCGAAGAC
-8 S I A T N A Y A E V Q L V E S G G L V Q P G G S L R L S C A A S G
    ^start of heavy chain

101 GCTTCACCAT TAGTAATTAT GGGATACACT GGGTGCGTCA GGGCCCGGGT AAGGGCTGG TAGGATTCT CCTTCTAACG GCTCTACTTA
    CGAAGTGGTA ATCATTAATA CCCATGTGA CCCACGCACT CCGGGGCCCA TTCCCGGACC TTACCCAACC ATCTAAAGA GGAAGATTGC CGAGATGAAT
27 F T I S N Y G I H W V R Q A P G K G L E W V G R I S P S N G S T Y
    ^CDR-H2

101 CTATGCCCGAT AGCGTCAAG GCGTTTCAC TATAAGCGCA GACACATCCA AAAACACAGC CTACCTACAA ATGAACAGCT TAAGAGCTGA GGACACTGCC
    GATACGGCTA TCGCAGTTCC CGGCAAGTG ATATTGCGGT CTGTGTAGGT TTTGTGTGCG GATGGATGTT TACTGTGCGA ATTCTCGACT CCTGTGACGG
60 Y A D S V K G R F T I S A D T S K N T A Y L Q M N S L R A E D T A

201 GTCTATTATT GTGCAAAATG CTCGGTCAGG TTCGGTTACT GGGGTCAAGG AACACTAGTC ACCGTCTCCT CGGCCTCCAC CAAGGCCCA TCGGTCTTCC
    CAGATAATAA CAGGTTTAC GAGCCAGTCC AAGCGAATGA CCCCAGTTCC TTGTGATCAG TGGCAGAGGA GCGGAGGTG GTTCCCGGGT AGCCAGAAGG
93 V Y Y C A K C S V R F A Y W G Q G T L V T V S S A S T K G P S V F P
    ^CDR-H3

```

FIG. 28b



101 CCCTGGCACC CTCCTCCCAAG AGCACCTCTG GGGGCACAGC GGGCTGGGC TGCCCTGGTCA AGGACTACTT CCCCGAACCG GTGACGGTGT CGTGGAACTC  
GGGACCGTGG GAGGAGGTTT TCGTGGAGAC CCCCCTGTTCG CCGGGACCCG ACGGACCACT TCGTATGAA GGGGCTGGC CACTGCCACA GCACCTTGAG  
27 L A P S S K S T S G G T A A L G C L V K D Y F P E P V T V S W N S  
  
01 AGCGGCCCTG ACCAGCGGCG TGCACACCTT CCGGCTGTCT CTACAGTCTT CAGGACTCTA CTCCCTCAGC AGCGTGGTGA CCGTGCCCTC CAGCAGCTTG  
TCCGCGGGAC TGGTCCCGC ACGTGTGAA GGGCCGACAG GATGTGAGG GAGGAGTGC TCGCACCCTT GGCACGGGAG GTCGTGGAAC  
60 G A L T S G V H T F P A V L Q S S G L Y S L S S V V T V P S S S L  
  
01 GGCACCCAGA CCTACATCTG CAACGTGAAT CACAAGCCCA GCAACACCAA GGTGACAAAG AAGTTGAGC CCAATCTTG TGACAAAAC CACCTCAGTG  
CCGTGGGTCT GGATGTAGAC GTTGCACTTA GTGTTCGGGT CGTGTGGGT CCAGCTGTTT CCACTGTTTGA ACTGTTTGA GTGGAGTCA  
93 G T Q T Y I C N V N H K P S N T K V D K K V E P K S C D K T H L S G  
start of gene III coat protein (267-end)  
^end of heavy chain  
  
01 GCGGTGGCTC TGGTTCGGT GATTGTGATT ATGAAAAGAT GGAACACGCT AATAAGGGG CTATGACCGA AATGCGCAT GAAACGGCG TACAGTCTGA  
CGCCACCGAG ACCAAGGCCA CTAATACTAA TACTTTCTA CCGTTTGGG TTTATCCCC GATCTGGCT TTTACGGCTA CTTTGGCGG ATGTCAGACT  
17 G G S G S G D F D Y E K M A N A N K G A M T E N A D E N A L Q S D  
37/75  
  
01 CGCTAAAGGC AAATCTGATT CTCTCGCTAC TGATTACGGT GCTGCTATCG ATGTTTCTAT TGGTGACGTT TCCGGCCTTG CTAATGGTAA TGGTGCTACT  
GCCATTCCG TTGTAAGTAA GACAGCGATG ACTAATGCCA CGACGATAGC TACCAAGTAA ACCACTGCAA AGGCGGAAC GATTACCATT ACCACGATGA  
60 A K G K L D S V A T D Y G A A I D G F I G D V S G L A N G N G A T  
  
01 GGTGATTGTG CTGCTCTAA TTCCCAAATG GCTCAAGTGC GTGACGGTGA TAATTCACCT TTAATGAATA ATTTCGGTCA ATATTACCT TCCCTCCCTC  
CCACTAAAC GACCGAGATT AAGGTTTAC CGAGTTCAGC CACTGCCACT ATTAAGTGA AATTACTTAT TAAAGCAGT TATAAATGA AGGAGGGAG  
93 G D F A G S N S Q M A Q V G D G D N S P L M N N F R Q Y L P S L P Q  
  
01 AATCGGTGA ATGTCGCCCT TTTGTCTTTA GGGCTGGTAA ACCATATGA TTTTCTATTG ATTGTGACAA AATAAACTTA TTCCGTGGTG TCTTTGCGTT  
TTAGCCAACT TACAGCGGGA AAACAGAAAT CCGGACCATT TGGTATACCT AAAAGATAAC TAACACTGTT TTAATTGAAT AAGGCACCAC AGAAACGCAA  
27 S V E C R P F V F S A G K P Y E F S I D C D K I N L F R G V F A F  
  
01 TCTTTTATAT GTTCCACCT TTATGTATGT ATTTTCTACG TTTGCTAACA TACTGGCTAA TAAGAGTCT TAA  
AGAAATATA CAACGGTGA AATACATACA TAAAGATGC AAACGATTGT ATGACCATTT ATTCCTCAGA ATT  
60 L L Y V A T F M Y V F S T F A N I L R N K E S O

1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTGCG TTTTTCAT TGCTACAAAT GCCTATGCAT CCGATATCCA GATGACCCAG TCCCAGAGCT  
 TACTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTA CCGATACGTA GGCTATAGGT CTACTGGGTC AGGGGCTCGA  
 1 M K K N I A F L L A S M F V F S I A T N A Y A S D I Q M T Q S P S S  
 ^met  
 ^start of stII signal sequence  
 ^light chain start  
 101 CCTGTCCGC CTCGTGGGC GATAGGGTCA CCATCACCTG CCGTGCAGT CAGGATGTGT CCACTGCTGT AGCCTGGTAT CAACAGAAAC CAGAAAAGC  
 GGCACAGCG GAGACACCG CTATCCAGT GGTAGTGGAC GGCACGGTCA GTCTACACA GGTGACGACA TCGGACCATA GTTGTCTTTG GTCCTTTTCG  
 35 L S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K P G K A  
 ^CDR-L1  
 201 TCCGAAGCTT CTGATTACT CGGCATCCTT CCTTACTCT GGAGTCCCTT CTGCTTCTC TGGTAGCGGT TCCGGGACGG ATTCACTCT GACCATCAGC  
 AGGCTTCGAA GACTAAATGA GCCGTAGGAA GGAGATGAGA CCTCAGGGAA GAGCGAAGAG ACCATCGCCA AGGCCCTGCC TAAAGTGAGA CTGGTAGTCG  
 68 P K L L I Y S A S F L Y S G V P S R F S G S G S G T D F T L T I S  
 ^CDR-L2  
 301 AGTCTGCAGC CGGAAGACTT CGCAACTTAT TACTGTGAGC AATCTTATAC TACTCTCCC ACCTTCGGAC AGGGTACCAA GGTGGAGATC AAACGAATG  
 TCAGACGTCG GCCTTCTGAA GCGTTGAATA ATGACAGTCG TTAGAATATG ATGAGGAGGG TCGAAGCCTG TCCATGGTT CCACCTCTAG TTTGCTTAC  
 101 S L Q P E D F A T Y Y C Q Q S Y T T P P T F G Q G T K V E I K R T V  
 ^CDR-L3  
 401 TGGCTGCACC ATCTGTCTTC ATCTTCCCGC CATCTGATGA GCAGTTGAAA TCTGGAACCTG OCTCTGTTGT GTGCTGCTG AATAACTTCT ATCCCAGAGA  
 ACCGACGTGG TAGACAGAAG TAGAAGGGCG GTAGACTACT CGTCAACTTT AGACCTTGAC GGAGACAACA CACGGACGAC TTATGAAGA TAGGCTCTCT  
 135 A A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E  
 501 GGCCAAAGTA CAGTGAAGG TGGATAACGC CCTCAATCG GGTAACTCC AGGAGAGTGT CACAGAGCAG GACAGCAAG ACAGCACCTA CAGCCTCAGC  
 CCGGTTTCAT GTCACCTTCC ACCTATTGCG GGAGGTAGC CCATTGAGG TCTCTCACA GTGTCTCGTC CTGCTGTTCC TGTCGTGGAT GTCGGAGTCG  
 168 A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S  
 601 AGCACCTTGA CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC CTGCGAAGTC ACCCATCAGG GCCTGAGTTC GCCCGTCACA AAGAGCTTCA  
 TCGTGGGACT GCGACTCGTT TCGTCTGATG CTCTTTGTGT TTCAGATGCG GACGCTCAG TGGGTAGTCC CGGACTCGAG CGGGCAGTGT TTCTCGAAGT  
 201 S T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N

FIG.- 29 A

```

11 ACAGGGGAGA GTGTGGTGCC AGCTCCGGTA TGCTGATCC GAACCGTTTC CGCGGTAAGG ACCTGGCATA ACTCGAGGCT GATCCTCTAC GCCGGACGCA
TGTCCCTCTCT CACACACAGG TCGAGGCCAT ACCGACTAGG CTTGGCAAG GCGCCATTC TGGACCGTAT TGAGCTCCGA CTAGGAGATG CCGCCTGCGT
15 R G E C G A S S G M A D P N R F R G K D L A O
^end of light chain, start of gD tag

11 TCGTGGCCCT AGTACGCAAG TTCACGTAAG AAGGGTAACT AGAGGTGAG GTGATTTTAT GAAAAAGAAT ATCGCATTTT TTCTTGCAATC TATGTTCTGTT
AGCACCGGGA TCATGGGTTTC AAGTGCAATTT TTCCCATTTGA TCTCCAACTC CACTAAATAA CTTTTCCTTA TAGCGTAAAG AAGAACGTAG ATACAAGCAA
13 M K K N I A F L L A S M F V
^start of stII

11 TTTTCTATTG CTACAAACGC GTACGCTGAG GTTCAGCTGG TGAGTCTGG CGGTGGCCTG GTGCAGCCAG GGGGCTCACT CCGTTTGCTC TGTGCAGCTT
AAAAGATAAC GATGTTTGG CATGCGACTC CAAGTCGACC ACCTCAGACC GCCACCGGAC CACGTCGCTC CCCCAGAGTGA GGCAACACAGG ACACGTCGAA
19 F S I A T N A Y A E V Q L V E S G G L V Q P G G S L R L S C A A S
^start of heavy chain ^CDR-H1

11 CTGGCTTCAC CATTAAGTGGT TCTGATATAC ACTGGGTGCG TCAGGCCCCG GGTAAAGGCC TGGATGGGT TGGTAGGATT TCTCCTTATG GCGGCAATAC
GACCGAAGTG GTAATCACCA AGACTATATG TGACCCACGC AGTCCGGGGC CCATTCCTGG ACCTTACCCA ACCATCTCTAA AGAGGAATAC CGCCGTTATG
39/75 6 G F T I S G S D I H W V R Q A P G K G L E W V G R I S P Y G G N T
^CDR-H2

11 TAACTATGCC GATAGCGTCA AGGCCCGTTT CACTATAAGC GCAGACACAT CCATAAACAC AGCCTACCTA CAAATGAACA GCTTAAGAGC TGAGGACACT
ATTGATACGG CTATCGCAGT TCCCGGGCAA GTCTGTGTA GGTTTTGTG TCGGATGGAT GTTTACTTGT CGAATTCTCG ACTCCTGTGA
19 N Y A D S V K G R F T I S A D T S K N T A Y L Q M N S L R A E D T

11 GCCGTCTATT ATTGTGCAAG AGTCGGCGGC CTCAAGTTGC TGTTCGACTA CTGGGGTCAA GGAACACTAG TCACCGCTCTC CTCGGCCCTCC ACCAAGGGCC
CGGCAGATAA TAACACGTTT TCAGCCGCGG GAGTTCAACG ACAAGCTGAT GACCCAGTT CATTCTGATC AGTGGCAGAG GAGCCGGAGG TGGTTCCCGG
2 A V Y Y C A R V G G L K L L F D Y W G Q G T L V T V S S A S T K G P
^CDR-H3

11 CATCGGTCCT CCCCTGGCA CCTCTCTCCA AGAGCACCTC TGGGGGCACA GCGGCCCTGG GTTCCCTGGT CAAGGACTAC TTCCCCGAAC CGGTGACGGT
GTAGCCAGAA GGGGGACCGT GGGAGGAGGT TCTCGTGGAG ACCCCCGTGT CCGCGGGACC CGAGGGACCA GTTCTGATG AAGGGGCTG GCCACTGCCA
6 S V F P L A P S S K S T S G G T A A L G C L V K D Y F P E P V T V

```

FIG. 29B

1401 GTGGTGAAC TCAGGGGCCC TGACCAGCGG CGTGCACACC TTCCGGGCTG TCCTACAGTC CTCAGGACTC TACTCCCTCA GCAGCGTGGT GACCGTGCCC  
 CAGCACCTTG AGTCCGGGGG ACTGGTCGCC GCACGTGTGG AAGGCCGAC AGGATGTCAG GAGTCTCTGAG ATGAGGGAGT CGTCGCCACCA CTGGCAGCGG  
 159 S W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V T V P  
 1501 TCCAGCAGCT TGGGACCCCA GACCTACATC TGCAACGTGA ATCACAAGCC CAGCAACACC AAGGTCGACA AGAAAGTTGA GCCCAAATCT TGTGACAAAA  
 AAGTCGTGCA ACCCGTGGT CTGGATGTAG ACGTTGCACT TAGGTTCGG GTCTGTGGG TTCCAGCTGT TCTTTCAACT CGGGTTTGA ACACCTGTTTT  
 192 S S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S C D K T  
 1601 CTCACGGCGC CATGAAACAG CTAGAGGACA AGGTGGAAGA GCTACTCTCC AAGAACTACC ACCTAGAGAA TGAAGTGGA AGACTCAAAA AACTTGTCTGG  
 GAGTGCCGGC GTACTTTGTC GATCTCCTGT TCCAGCTTCT CGATGAGAGG TTCTTGTATGG TGGATCTCTT ACTTCACCGT TCTGAGTTTT TTGAACAGCC  
 226 H G R M K Q L E D K V E L L S K N Y H L E N E V A R L K K L V G  
 ^end of heavy chain, start of leucine zipper  
 1701 GGAGCGCGGA AAGCTTAGTG GCGGTGGCTC TGGTTCGGT GATTTTGATT ATGAAAAGAT GGCAAAAGCT AATAAGGGGG CTATGACCGA AAATGCCGAT  
 CCTCGCGCCT TTCGAATCAC CGCCACCCGAG ACCAAGGCCA CTAAAACTAA TACTTTTCTA CCGTTTCCGA TTATTCCCCC GATACTGGCT TTTACGGCTA  
 259 E R G K L S G G S G S G D F D Y E K M A N A N K G A M T E N A D  
 ^end of leucine zipper, gene III coat protein (267-end)  
 1801 GAAAACGCGC TACAGTCTGA CGCTAAAGGC AAACCTTGATT CTCTCGCTAC TGATPACGGT GCTGCTATCG ATGGTTTCAT TGGTGACGTT TCCGGCCCTG  
 CTTTTCGGCG ATGTCAGACT GCGATTTCCG TTTGAACTAA GACAGCGATG ACTAATGCCA CGACGATAGC TACCAGAGTA ACCACTGCAA AGGCCGGAAC  
 292 E N A L Q S D A K G K L D S V A T D Y G A A I D G F I G D V S G L A  
 1901 CTAATGGTAA TGGTGTACT GGTGATTTTG CTGGCTCTAA TTCCCAATG GCTCAAGTCG GTGACGGTGA TAATTCACCT TTAATGAATA ATTTCGGTCA  
 GATTACCAT ACCACGATGA CCACCTAAAC GACCGAGATT AAGGTTTAC CGACTTCAGC CACTGCCACT ATTAAGTGA AATTACTTAT TAAAGGCAGT  
 326 N G N G A T G D F A G S N S Q M A Q V G D G D N S P L M N N F R Q  
 2001 ATATTACCT TCCCTCCCTC AATCGGTTGA ATGTGCGCCT TTTGTCTTTA GCGGTGGTAA ACCATATGAA TTTTCTATTG ATTGTGACAA AATAAACCTA  
 TATAAATGGA AGGAGGGGAG TTAGCCCACT TACAGCGGGA AAACAGAAAT CCGGACCATT TGGTATACTT AAAAGATAAC TAACACTGTT TTATTGTAAT  
 359 Y L P S L P Q S V E C R P F V F S A G K P Y E F S I D C D K I N L  
 2101 TTCCGTGGTG TCTTTGCGTT TCTTTTATAT GTTGCCACCT TTATGTATGT ATTTTCTACG TTTGCTAACA TACTGCGTAA TAAGGAGTCT TAA  
 AAGGCACCAC AGAAACGCAA AGAAATATA CAACGGTGA AATACATACA TAAAGATGC AAACGATTGT ATGACGCATT ATTCCTCAGA ATT  
 392 F R G V F A F L L Y V A T F M Y V F S T F A N I L R N K E S O

FIG. 29C

1 ATGAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTCTCTAT TGCTACAAAT GCCTATGCGT CCGATATCCA GATGACCCAG TCCCCGAGCT  
TACTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATCTTTA CCGATACGTA GGCTATAGST CTACTGGGTC AGGGGCTCGA  
 1 M K K N I A F L L A S M F V F S I A T N A Y A S D I Q M T Q S P S S  
 ^start of stII signal sequence  
 ^met  
 ^light chain start

101 CCCTGTCCGC CTCTGTGGGC GATAGGGTCA CCATCACCTG CCGTGCCAGT CAGGATGTGT CCACGTCTGT AGCCTGGTAT CAACAGAAAC CAGGAAAAGC  
 GGGACAGGCG GAGACACCCG CTATCCCACT GGTAGTGGAC GGCACGGTCA GTCTACACA GGTGAGGACA TCGGACCATA GTTGTCTTTG GTCTTTTTCG  
 35 L S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K P G K A  
 ^CDR-L1

201 TCCGAAGCTT CTGATTACT CGGCATCCTT CCTCTACTCT GGAGTCCCTT CTGCTTCTC TGCTAGCGGT TCCGGGACGG ATTTCACTCT GACCATCAGC  
 AGGCTTCGAA GACTAAATGA GCCGTAGGAA GGAGATGAGA CCTCAGGGA GAGCGAAGAG ACCATCGCCA AGGCCCTGCC TAAAGTGAGA CTGGTAGTCG  
 68 P K L L I Y S A S F L Y S G V P S R F S G S G T D F T L T I S  
 ^CDR-L2

301 AGTCTGCAGC CGGAAGACTT CGCAACTTAT TACTGTGAGC AATCTTATAC TACTCCTCCC AGTTCGGAC AGGTACCAA GGTGAGATC AAACGAACTG  
 TCAGACGTCG GCCTTCTGAA GCGTTGAATA ATGACAGTCG TTAGAATATG ATGAGGAGGG TGCAAGCCTG TCCCATGGTT CCACCTCTAG TTTGCTTGAC  
 101 S L Q P E D F A T Y Y C Q Q S Y T T P P T F G Q G T K V E I K R T V  
 ^CDR-L3

401 TGGCTGCACC ATCTGTCTTC ATCTTCCCGC CATCTGATGA GCAGTTGAAA TCTGGAACTG CCTCTGTTGT GTGCTGTCTG AATACTTCT ATCCAGAGA  
 ACCGACGTGG TAGACAGAAG TAGAAGGGCG GTAGACTACT CGTCAACTTT AGACCTTGAC GGAGACAACA CACGGACGAC TTATTGAAGA TAGGCTCTCT  
 135 A A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E

501 GGCCAAAGTA CAGTGGAGG TGGATAACGC CCTCCAATCG GGTAACCTCC AGGAGAGTGT CACAGAGCAG GACAGCAAGG ACAGCACCTA CAGCCTCAGC  
 CCGGTTTCAT GTCACCTTCC ACCTATTGCG GGAGGTTAGC CCATTGAGGG TCCTCTCACA GTGCTCTGTC CTGCTCGTTCC TGTCGTGGAT GTCGGAGTCG  
 168 A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S

601 AGCACCCCTGA CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC CTGCGAAGTC ACCATCAGG GCCTGAGTC GCCCGTCACA AAGAGCTTCA  
 TCGTGGGACT GCGACTCGTT TCGTCTGATG CTCTTTGTGT TTCAGATCGG GACGCTTCAG TGGTAGTCC CCGACTCAG CCGGCAGTGT TTCTCGAAGT  
 201 S T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N

FIG. 30A

701 ACAGGGGAGA GTGTGGTGCC AGCTCCGGTA TGGCTGATCC GAACCGTTTC CGCGTAAGG ACCTGGCATA ACTCGAGGCT GATCCTCTAC GCCGGACGCA  
 TGTCCCTCT CACACCACGG TCGAGGCCAT ACCGACTAGG CTTGGCAAG GCGCATTC TGGACCGTAT TGAGCTCGA CTAGAGATG CGGCCCTGGT  
 35 R G E C G A S S G M A D P N R F R G K D L A O  
 ^end of light chain, start of gD tag

101 TCGTGGCCCT AGTACGCAAG TTCACGTAAG AAGGGTAACT AGAGTTGAG GTGATTTTAT GAAAAAGAT ATCGCATTC TTCTTGCATC TATGTTCTGT  
 AGCACCGGGA TCATGCGTTC AAGTGCATTT TTCCCATTTGA TCTCCAACTC CACATAAATA CTTTTTCTTA TAGCGTAAAG AAGAACGTAG ATACAAGCAA  
 23 M K K N I A F L L A S M F V  
 ^start of still

01 TTTTCTATTG CTACAAACGC GTACGCTGAG GTTCAGCTGG TGGAGTCTGG CGGTGGCCTG GTGCAGCCAG GGGGCTCACT CCGTTTGTCC TGTGCAGCTT  
 AAAAGATAAC GATGTTTGG CATGCGACTC CAAGTCGACC ACCTCAGACC GCCACCGGAC CAGTCGGTC CCCCGAGTGA GGCAACAGG ACACGTCGAA  
 -9 F S I A T N A Y A E V Q L V E S G G L V Q P G G S L R L S C A A S  
 ^start of heavy chain

01 CTGGCTCAC CATTACTAAT TCCGATATAC ACTGGTGCG TCAGGCCCGG GGTAAGGCC TGAATGGGT TGCTACTATT TATCCTTATG GCGGCTATAC  
 GACGAAGTG GTAATGATTA AGGCTATATG TGACCCAGC AGTCCGGGCG CCATTCCCGG ACCTTACCCA AGCATGATAA ATAGAATAC CGCCGATATG  
 6 G F T I T N S D I H W V R Q A P G K G L E W V A T I Y P Y G G Y T  
 ^CDR-H2

11 TTACTATGCC GATAGGCTCA AGGGCCGTTT CACTATAAGC GCAGACACAT CCAAAACAC AGCCTACCTA CAAATGAACA GCTTAAGAGC TGAGGACACT  
 AATGATACGG CTATCGCAGT TCCCGGCATA GTGATATTGC CGTGTGTGA GGTGTTGTG TCGGATGGAT GTTTACTTGT CGAATCTCTG ACTCCTGTGA  
 19 Y Y A D S V K G R F T I S A D T S K N T A Y L Q M N S L R A E D T

11 GCCGTCTATT ATTGTGCAAG AGGGGGCGG ATGGACGGCT AGTTATGGA CTACTGGGGT CAAGGAACAC TAGTCACCGT CTCTCGGCC TCCACCAAGG  
 CGGCAGATAA TAACACGTTT TCCCGCGCC TACCTGCCGA TGCAATACCT GATGACCCCA GTTCCTTGTG ATCAGTGGA GAGGAGCCG AGGTGGTTCC  
 2 A V Y Y C A R G G G M D G Y V M D Y W G Q G T L V T V S S A S T K G  
 ^CDR-H3

1 GCCCATCGGT CTTCCCGCTG GCACCTCTCT CCAAGAGCAC CTCTGGGGG ACAGGGGCC TGGGTGCCT GGTCAAGGAC TACTTCCCCG AACCGGTGAC  
 CGGTAGCCA GAAGGGGAC CGTGGGAGGA GGTTCCTGTG GAGACCCCG TGTCCCGCGG ACCCGACGGA CCAGTCTCTG ATGAAGGGG TTGGCCACTG  
 6 P S V F P L A P S S K S T S G G T A A L G C L V K D Y F P E P V T

FIG. 30b

1401 GGTGTCGTGG AACTCAGCG CCCTGACCAG CGGCGTGCAC ACCTTCCCG CTGTCTTACA GTCTACTCCC TCAGCAGCGT GGTGACCGTG  
 CCACAGCACC TTGAGTCCGC GGGACTGCTC GCGGCACGTG TGGAGGGCC GACAGGATGT CAGGAGTCCT GAGATGAGG AGTCGTGCA CCACTGGCAC  
 159 V S W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V T V  
 1501 CCCTCCAGCA GCTTGGGCAC CCAGACCTAC ATCTGCAACG TGAATCACA GCGCAGCAAC ACCAAGTGG ACAAGAAAGT TGAGCCCAA TCTTGTGACA  
 GGGAGGTCGT CGAACCCGTG GGTCTGGATG TAGACGTTC ACTTAGTGT CGGGTCGTG TGGTTCAGC ACTGCGGTTT AGAACACTGT  
 192 P S S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S C D K  
 1601 AAACCTCAGG CCGCATGAAA CAGCTAGAG ACAAGTCTC AGAGCTACTC TCCAAGAACT ACCACCTAGA GAATGAAGT GCAAGACTCA AAAAATTTGT  
 TTTGAGTGCC GCGGTACTTT GTGAGTCTCC TGTTCAGCT TCTCGATGAG AGGTTCCTGA TGGTGGATCT CTTACTCTCAG CGTCTCTGAG TTTTGAACA  
 226 T H G R M K Q L E D K V E L L S K N Y H L E N E V A R L K K L V  
 'end of heavy chain, start of leucine zipper  
 1701 CGGGGAGCGC GGAAAGCTTA GTGGCGGTGG CTCTGGTTCC GGTGATTTTG ATTATGAAA GATGGCAAAC GCTAATAAGG GGGCTATGAC CGAAAATGCC  
 GCCCTCGCG CTTTTCGAAT CACCGCCACC GAGACCAAGG CCACATAAAC TAATACTTTT CTACCGTTTG CGATTAATCC CCCGATCTG GCTTTTACGG  
 259 G E R G K L S G G S G S G D F D Y E K M A N A N K G A M T E N A  
 'end of leucine zipper, start of gene III coat protein (267-end)  
 801 GATGAAAACG CGCTACAGTC TGACGTAAA GGCAAACTTG ATCTGTGCG TACTGATTAC GGTCTGCTA TCGATGGTTT CATTTGGTGAC GTTTCGGGCC  
 CTAATTTTGC GCGATGTCAG ACTGCGATTT CCGTTTGAAC TAAGACAGCG ATGACTAATG CCACGACGAT AGCTACCAA GTAACCACTG CAAAGGCCGG  
 292 D E N A L Q S D A K G K L D S V A T D Y G A A I D G F I G D V S G L  
 1901 TTGCTAATGG TAAFGGTGCT TTGCTGGCTC TAATTCOCOA ATGGCTCAAG TCGGTGACGG TGATAATTCA CCTTAATGA ATAAATTTCCG  
 AACGATTACC ATTACACGGA TGACCACCTAA AAGACCGAG ATTAAGGTT TACCGAGTTC AGCCACTGCC ACTATTAGT GGAAATTAAT TATTAAAGGC  
 326 A N G N G A T G D F A G S N S Q M A Q V G D G D N S P L M N N F R  
 2001 TCAATATTTA CCTTCCCTCC CTCAATCGGT TGAATGTGC CCTTTTGTCT TTAGCGGTGG TAAACCAAT GAATTTTCTA TTGATTGTGA CAAAATAAAC  
 AGTTATAAAT GGAAGGGAGG GAGTTAGCCA ACTTACAGCG GGAACACAGA AATCGGACC ATTTGGTATA CTTAAAAGAT AACTAACACT GTTTTATTG  
 359 Q Y L P S L P Q S V E C R P F V F S A G K P Y E F S I D C D K I N  
 2101 TTATTCCGFG GTGTCTTTTC GTTCTTTTTA TATGTTGCCA CCTTTATGTA TGTATTTTCT ACCTTTTCTA ACATACCTGG TAATAAGGAG TCTTAA  
 AATAAGGCAC CACAGAAAACG CAAAGAAAAT ATACAACGGT GGAATAACAT ACATAAAGA TGCAACGAT TGTATGACCG ATTATTCTC AGAATT  
 392 L F R G V F A F L L Y V A T F M Y V F S T F A N I L R N K E S O

FIG. 30C

```

1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCTG TTTTTCCTAT TGCTACAAAT GCCTATGCAT CCGATATCCA GATGACCCAG TCCCCGAGCT
TACTTTTCTT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAGATA ACATGTTTA CCGATACGTA GGCTATAGGT CTACTGGGTC AGGGGCTCGA
1 M K K N I A F L L A S M F V F S I A T N A Y A S D I Q M T Q S P S S
^met ^light chain start

101 CCCTGTCCGC CTCTGTGGC GATAGGTCA CCATCACCTG CCGTGCCAGT CAGGATGNGT CCACTGCTGT AGCCTGGTAT CAACAGAAAC CAGGAAAAGC
GGGACAGCG GAGACACCCG CTATCCAGT GGTAGTGGAC GGCACGGTCA GTCCTACACA GGTGACGACA TCGGACCATA GTTGTCTTTG GTCTTTTTCG
35 L S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K P G K A
^CDR-L1

201 TCCGAAGCTT CTGATTTACT CGGCATCCTT CCTCTACTCT GGAGTCCCTT CTGGCTTCTC TGGTAGCGGT TCCGGGACGG ATTCACTCT GACCATCAGC
AGGCTTCGAA GACTAAATGA GCCGTAGGAA CCGATGAGGA GAGCGAAGAG ACCATCGCCA AGGCCCTGCC TAAAGTGAGA CTGCTAGTCCG
68 P K L L I Y S A S F L Y S G V P S R F S G S G T D F T L T I S
^CDR-L2

301 AGTCTGCAGC CGGAAGACTT CGCAACTTAT TACTGTGAGC AATCTTATAC TACTCCCTCC ACCTTCGGAC AGGTACCAA GGTGGAGATC AAACGAACTG
TCAGACGTGG GCCTTCGAA GCGTTGAAAT ATGACAGTGC TTAGAATATG ATGAGGAGGG TGCAAGCCTG TCCCATGGTT CCACCTCTAG TTGCTTGAC
101 S L Q P E D F A T Y Y C Q Q S Y T T P P T F G Q G T K V E I K R T V
^CDR-L3

401 TGGCTGCACC ATCTGTCTTC ATCTTCCGC CATCTGATGA GCAGTTGAAA TCTGGAATG CCTCTGTGT GTGCCCTGCTG AATAACTTCT ATCCCAGAGA
ACCGACGTGG TAGACAGAAG TAGAAGGGCG GTAGACTACT CGTCAACTTT AGACCTTGAC GGAGACACAA CACGGACGAC TTATTGAAGA TAGGGTCTCT
135 A A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E

501 GGCCAAAGTA CAGTGAAGG TGGATAACG CCTCCAATCG GGTAACTCC AGGACAGTGT CACAGAGCAG GACAGCAAGG ACAGCACCTA CAGCCTCAGC
CCGGTTTCAT GTCACTTCC ACCATTTGG GGAGGTTAGC CCATTGAGG TCCTCTCACA GTGTCTCGTC CTGTCTGTC TGTCTGGAT GTCCGAGTCCG
168 A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S

601 AGCACCCCTGA CCGTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACG CTGCGAAGTC ACCCATCAGG GCCTGAGCTC GCCCGTCACA AAGAGCTTCA
TCGTGGGACT GCAGCTCGTT TCGTCTGATG CTCTTTGTGT TTCAGATGG GACCTTCAG TGGGTAGTCC CCGACTCGAG CGGGCAGTGT TTCTCGAAGT
201 S T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N

```

FIG. 31A



11 ACAGGGGAGA GTGTGGTGCC AGCTCCGGTA TGGGTGATCC GAACCGTTTC CGCGGTAAGG ACCTGGCATA ACTCGAGGCT GATCCTCTAC GCCGGACGCA  
 TGTCCCTCTT CACACCAAGG TCGAGGCCAT ACCGACTAGG CTTGGCAAG GCGCCATTCC TGGACCGTAT TGAGCTCCGA CTAGGAGATG CCGCCTGCGT  
 15 R G E C G A S S G M A D P N R F R G K D L A O  
 ^end of light chain, start of gD tag  
 11 TCGTGGCCCT AGTACGCAAG TTCACGTAAA AAGGGTAACT AGAGGTGAG GTGATTATAT GAAAAAGAAAT ATCGCATTTT TTCTTGCAATC TATGTTTCGTT  
 AGCACCGGGA TCATGCGTTC AAGTGCAATTT TTCCCATTTA TCCTCAACTC CACTAAAATA CTTTTCCTTA TAGCGTAAAG AAGAACGTAG ATACAAGCAA  
 13 M K K N I A F L L A S M F V  
 ^start of still  
 1 TTTTCTATTG CTACAAACGC GTACGCTGAG GTTCAGCTGG TGGAGTCTGG CCGTGGCCTG GTGCAGCCAG GGGGCTCACT CCGTTTGTC TGTGCAGCTT  
 AAAAGATAC GATGTTTGG CATGCGACTC CAAGTCGACC ACCTCAGACC GCCACGGGAC CACGTCGGTC CCCCAGGTGA GGCAACAGG ACACGTCGAA  
 9 F S I A T N A Y A E V Q L V E S G G L V Q P G G S L R L S C A A S  
 ^start of heavy chain ^CDR-H1  
 1 CTGGCTTCAC CATTAATAAT TATGATATAC ACTGGGTGCG TCAGGCCCGG GGTAAAGGCC TGGATGGGT TGGTTATATT TCTCTCTCCTA GCGGGCGTAC  
 GACCGAAGTG GTAATTATTA ATACTATATG TGACCCACGC AGTCCGGGGC CCATTCCCGG ACCTTACCCA ACCAATATAA AGAGGAGGAT CGCCGCGATG  
 ; G F T I N N Y D I H W V R Q A P G K G L E W V G Y I S P P S G A T  
 ^CDR-H2  
 1 TTACTATGCC GATAGCGTCA AGGGCGGTTT CACTATAAGC GCAGACACAT CCAAAAACAC AGCTACCTA CAAATGAACA GCTTAAAGAGC TGAGGACACT  
 AATGATACGG CTATCGCAGT TCCCGGCAAA GTGATATTG CGTCTGTGTA GGTTTTGTG TCGGATGGAT GTTTACTTGT CGAATTCTCG ACTCCTGTGA  
 9 Y Y A D S V K G R F T I S A D T S K N T A Y L Q M N S L R A E D T  
 1 GCCGTCTATT ATTGTGCAAG AATGTCGGC ATGCGGAGGG GGGTTATGGA CTACTGGGGT CAAGGAACAC TAGTCACCGT CTCCTCGGCC TCCACCAAGG  
 CGGCAGATAA TAACACGTTT TTACCAGCCG TAGCGCTGCC CCAATACCT GATGACCCCA GTTCCTTGTG ATCAGTGGCA GAGGAGCCGG AGGTGTTCC  
 2 A V Y Y C A R M V G M R R G V M D Y W G Q G T L V T V S S A S T K G  
 ^CDR-H3  
 1 GCCCATCGGT CTTCCTCCCTG GCACCTCTCT CCAAGAGCAC CTCTGGGGC ACAGGGGCC TGGGCTGCCT GGTCAAGGAC TACTTCCCCG AACCGGTGAC  
 CGGGTAGCCA GAAGGGGGAC CGTGGGGAGG GGTTCCTGTTG GAGACCCCG TGTGCGCCGG ACCCGACGGA CCAGTTCCTG ATGAAGGGGC TTGGCCACTG  
 6 P S V F P L A P S S K S T S G G T A A L G C L V K D Y F P E P V T

FIG. 31B

1401 GGTGTCGTGG AACTCAGGCG CCCTGACCAG CGGCGTGAC ACCTTCCCGG CTGTCTTACA GTCTACTCCC TCAGACGCGT GGTGACCGTG  
 CCACAGCACC TTGAGTCCGC GGGACTGCTC GCGGCACGTG TGAAGGGCC GACAGGATGT CAGGAGTCTT GAGATGAGG AGTCGTGCA CCACTGGCAC  
 159 V S W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V T V  
 1501 CCCTCCAGCA GCTTGGGCAC CCAGACCTAC ATCTGCAACG TGAATCACA GCCAGCAAC ACCAAGTCTG ACAAGAAAGT TGAGCCCCAA TCTTGTGACA  
 GGGAGGTCTG CGAACCCTGT GGTCTGGATG TAGACGTTGC ACTTAGTGT CCGGTCTGTT TGGTCCAGC TGTCTCTTCA ACTCGGGTTT AGAACACTGT  
 192 P S S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S C D K  
 1601 AAACCTCAGG CCGCATGAAA CAGCTAGAGG ACAAGGTGCA AGAGCTACTC TCACAAGACT ACCACCTAGA GAATGAAGTG GCAAGACTCA AAAAATTTGT  
 TTTGAGTGCC GGGGTACTTT GTGATCTTCC TGTTCAGCT TCTCGATGAG AGGTTCTTGA TGGTGGATCT CTTACTTCAC CGTCTGAGT TTTTGAACA  
 226 T H G R M K Q L E D K V E L L S K N Y H L E N E V A R L K K L V  
 ^end of heavy chain, start of leucine zipper  
 1701 CGGGGAGCGC GGAAAGCTTA GTGGCGGTGG CTCTGTTTCC GGTGATTTTG ATTATGAAA GATGGCAAC GCTAATAAGG GGGCTATGAC CGAAAATGCG  
 GCCCTCGCGC CCTTTCGAAT CACCGCCACC GAGACCAAGG CCACATAAAC TAATACTTTT CTACCGTTTG CGATTATTC CCCGATACTG GCTTTTACGG  
 259 G E R G K L S G G S G S G D F D Y E K M A N A N K G A M T E N A  
 ^end of leucine zipper  
 ^gene III coat protein (267-end)  
 1801 GATGAAAACG CGCTACAGTC TGACGCTAAA GGCAAACTTG ATCTGTGTCG TACTGATTAC GGTGCTGCTA TCGATGGTTT CATTTCCGGCC  
 CTACTTTTGC GCGATGTCAG ACTGCGATTT CCGTTTGAAC TAAGACAGCG ATGACTAATG CCACGACGAT AGCTACCAAA GTAACCACTG CAAAGGCCGG  
 292 D E N A L Q S D A K G K L D S V A T D Y G A A I D G F I G D V S G L  
 1901 TTGCTAATGG TAATGGTGT ACTGGTGATT TTGCTGGCTC TAATTTCCAA ATGGCTCAAG TCGGTGACGG TGATAATTCA CCTTTAATGA AFAATTTCCG  
 AACGATTACC ATTACACGA TGACCACCTAA AACGACCGAG ATTAAGGGTT TACCGAGTTC AGCCACTGCC ACTATTAACT GGAATTAAT TATTAAAGGC  
 326 A N G N G A T G D F A G S N S Q M A Q V G D G D N S P L M N N F R  
 2001 TCAATATTTA CCTTCCCTCC CTCAATCGGT TGAATGTGCG CCTTTGTCTT TTAGCGGTGG TAAACCATAT GAATTTTCTA TTGATTGTGA CAAAATAAAC  
 AGTTATAAAT GGAAGGGAGG GAGTTAGCCA ACTTACAGCG GGAAGACAGA AATCGCGACC ATTTGGTATA CTTAAAAGAT AACTAACACT GTTTTATTG  
 359 Q Y L P S L P Q S V E C R P F V F S A G K P Y E F S I D C D K I N  
 2101 TTATTCCGTG GTGTCTTTGC GTTTCTTTTA TATGTTGCCA CCTTTATGTA TGTATTCTT ACCTTTGCTA ACATACGCG TAATAAGGAG TCTTAA  
 AATAAGGCAC CACAGAAACG CAAAGAAAAT ATACAACGGT GGAATACAT ACATAAAGA TGCAACGAT TGTATGAGC ATTATTCCCTC AGAATT  
 392 L F R G V F A F L L Y V A T F M Y V F S T F A N I L R N K E S O

FIG. 31c

```

1  GAATTCAACT TCTCCATACT TTGGATAAGG AATAACAGAC ATGAAAATATC TCATTGCTGA GTTGTATTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT
   CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGTCTG TACTTTTATAG AGTAACGACT CAACAATAAA TTCGAACGGG TTTTCTTCT TCTCAGCTTA

101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATATG TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG
   CTTGACACAC GCGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CGCGTTTATC TGGTTGTGCG CAACTAACTA GTCCATCTCC

201 GGGCGCTGTA CGAGGTAAG CCCGATGCCA GCATTCCCTGA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA
   CCGCGGACAT GCTCCATTTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTTCACAA GCTGTCTATA AGTTGTACAG GCCGAGACTT ATAGTCGGTT TGTTTTATTT TTTTAATGTA TTTGTAACTA GTACGCAAGT
   TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAATAATA AAAATTACAT AAACATTGAT CATCGGTTCA

401 TCACGTAATA AGGCTATGTA GAGTTTGAGG TGATTTTATG AAAAGAATA TCGCAATTCT TCTTGCACTT ATGTTCTGTT TTTCTATTGC TACAAATGCC
   AGTGCATTTT TCCCATACAT CTCCAACCTC ACTAAAATAC TTTTCTTAT AGCGTAAAGA AGAACGTAGA TACAAGCAAA AAAGATAACG ATGTTTACGG

0      M K K N I A F L L A S M F V F S I A T N A
      ^start of stII signal sequence

501 TATGCAGATA TCAGATGAC CCAGTCCCGG AGCTCCCTGT CCGCTCTGT GGGCATAGG GTCACCATCA CCTGCCCTGC CAGTCAGGAT GTGTCCACTG
   ATACGTCTAT AGGTCTACTG GGTCAGGGGC TCGAGGGACA GGGGAGACA CCGGTATCC CAGTGTAGT GGACGGCAGG GTCAGTCCCTA CACAGGTGAC
21 Y A D I Q M T Q S P S S L S A S V G D R V T I T C R A S Q D V S T A
      ^start of light chain
      ^EcorV
      ^CDR-L1

601 CTGTAGCCTG GTATCAACAG AAACCAGGAA AAGCTCCGAA GCTTCTGATT TACTCGGCAT CCTTCTCTTA CTCTGGAGTC CCTTCTCGCT TCTCTGGTAG
   GACATCGGAC CATAGTTGTC TTTGGTCTTT TTTCGAGGCTT CGAAGACTAA ATGAGCCGTA GGAAGGAGAT GAGACCTCAG GGAAGAGCGA AGAGACCATC
55 V A W Y Q Q K P G K A P K L L I Y S A S F L Y S G V P S R F S G S
      ^CDR-L2

701 CGGTTCCGGG ACGGATTCA CTCGTACCAT CAGCAGTCTG CAGCCGGAAG ACTTCGCAAC TTATTACTGT CAGCAATCTT ATACTACTCC TCCCACGTTT
   GCCAAGGCC TGCCTAAAGT GAGACTGGTA GTCGTACAG GTCGGCCCTC TGAAGCGTTG AATAATGACA GTCGTTAGAA TATGATGAGG AGGTTGCAAG
88 G S G T D F T L T I S S L Q P E D F A T Y Y C Q Q S Y T T P P T F
      ^CDR-L3

```

FIG.-32A

1 GGACAGGGTA CCAAGGTGA GATCAAACGA ACTGTGGCTG CACATCTGT CTTCACTTC CCGCCATCTG ATGAGCAGTT GAAATCTGGA ACTGCCTCTG  
 CCTGTCCCAT GGTTCACCT CTAGTTTGGT TGACACCGAC GTGGTAGACA GAAGTAGAAG GCGGTAGAC TACTCGTCAA CTTTAGACCT TGACGGAGAC  
 1 G Q G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S V  
 ^KpnI  
 1 TTGTGTGCTT GCTGAATAAC TTCTATCCCA GAGAGGCCAA AGTACAGTGG AAGTGGATA ACGCCTCCA ATCGGTAAC TCCAGGAGA GTGTCACAGA  
 AACACACGGA CGACTTATTG AAGATAGGT CTCTCCGGT TCATGTCAAC TTCCACCTAT TCGCGAGGT TAGCCATTG AGGTCCTCT CACAGTGTCT  
 5 V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E  
 1 GCAGGACAGC AAGGACAGCA CCTACAGCCT CAGCAGCACC CTGACGCTGA GCAAAGCAGA CTACGAGAAA CACAAGTCT ACGCCTGCGA AGTCACCCAT  
 CGTCTCTGCG TTCCTGTCTG GGTCTCGGA GTCGTCTGG GACTCGGACT CGTTTCGTCT GATGCTCTTT GTGTTTCAGA TCGGACGCT TCAGTGGGTA  
 8 Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H  
 1 CAGGGCTGA GCTGCCCCGT CACAAAGAGC TTCAACAGG GAGAGTGTGG TGCCAGCTCC GGTATGGCTG ATCCGAACCG TTTCGCGGT AAGGACCTGG  
 GTCCCGGACT CGAGCGGCA GTGTTCTCG AAGTTCTCG AAGTTCTCG CACTACACC ACGTCTGAG CCATACCGAC TAGGCTGGC AAAGGCGCA TTCCTGGACC  
 Q G L S S P V T K S F N R G E C G A S S G M A D P N R F R G K D L A  
 ^end of light chain, start of gd tag  
 1 CAFAACTCGA GGCTGATCCT CTACGCCGGA CGCATCGTGG CCCTAGTAGC CAAGTTCACG TAAAAGGGT AACTAGAGGT TGAGGTGATT TTATGAAAAA  
 GTATTGAGCT CCGACTAGGA GATGCGGCTT GCGTAGCACC GGTCAAGTC GTTTTCCCA TTGATCTCCA ACTCCACTAA AATACITTTT  
 5 O  
 3 M K K  
 ^start of stII  
 1 GAATATCGCA TTTCCTCTTG CATCTATGTT CGTTTTTCTT ATTGCTACAA ACGGTACGC TGAGTTTCAG CTGGTGGAGT CTGGCGGTGG CCTGTGTCAG  
 CTTATAGCGT AAAGAAGAAC GTAGATACAA GCAAAAAAGA TAACGATGTT TGCGCATGG ACTCCAAGTC GACCACCTCA GACCGCCACC GGACACGTC  
 ) N I A F L L A S M F V F S I A T N A Y A E V Q L V E S G G G L V Q  
 ^start of heavy chain  
 ^BsiWi

FIG. 32b

1401 CCAGGGGGCT CACTCCGTTT GTCCTGTGCA GCTTCTGGCT TCACCATAG TGGTCTTGG ATACACTGGG TGGTCAAGC CCCGGGTAAG GGCCTGGAAT  
 GGTCCCCCGA GTGAGGCAAA CAGGACACGT CGAAGACCGA AGTGGTAATC ACCAAGAACC TATGTGACCC ACGCAGTCG GGGCCCATTC CCGGACCTTA  
 14 P G G S L R L S C A A S G F T I S G S W I H W V R Q A P G K G L E W  
 ^CDR-H1  
 1501 GGGTTGCTG GATTGCTCCT TATAGCGGG CTACTGACTA TGCGGATAGC GTCAGGGGCC GTTTCACATAT AAGCGCAGAC ACATCCAAAA ACACAGCCTA  
 CCCAACGAAC CTAACGAGGA ATATCGCGC GATGACTGAT ACGGCTATCG CAGTCCCGG CAAAGTGATA TTCCGCTCTG TGTAGGTTTT TGTGTCGGAT  
 48 V A W I A P Y S G A T D Y A D S V K G R F T I S A D T S K N T A Y  
 ^CDR-H2  
 1601 CCTACAAATG AACAGCTTAA GAGCTGAGGA CACTGCCGTC TATTATTGTG CAAGAGAGGG GGGCTGTGAC TGGGTGTTCG ACTACTGGG TCAAGGAACA  
 GGATGTTTAC TTGTGGAATT CTCGACTCCT GTGACGGCAG ATAATAACAC GTTCTCTCCC CCCGACATG ACCCACAAGC TGATGACCCC AGTTCTCTGT  
 81 L Q M N S L R A E D T A V Y Y C A R E G G L Y W V F D Y W G Q G T  
 ^CDR-H3  
 1701 CTAGTCACCG TCTCCTCGGC CTCCACCAAG GGCCCATCGG TCTTCCCCCT GGCACCTCC TCCAAGAGCA CCTCTGGGG CACAGCGGC CTGGGCTGCC  
 GATCAGTGGC AGAGGAGCG GAGTGGTTC CCGGTTAGCC AGAAGGGGA CCGTGGGAGG AGTTCTCTGT GGAGACCCCC GTGTGCGCGG GACCCGACGG  
 114 L V T V S S A S T K G P S V F P L A P S S K S T S G G T A A L G C L  
 ^ApaI  
 1801 TGGTCAAGGA CTACTTCCC GAACGGTGA CGGTGTCTGG GAACTCAGC GGCCTGACCA CGGCGGTGCA CACCTTCCC GCTGTCTTAC AGTCCTCAGG  
 ACCAGTTCTT GATGAAGGG CTTGGCCACT GCCACAGCAC CTTGAGTCCG CGGGACTGGT CGCCGACAGT GTGGAAGGGC CGACAGGATG TCAGGAGTCC  
 148 V K D Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S S G  
 1901 ACTCTACTCC CTCAGCAGCG TGGTGACCGT GCCCTCCAGC AGCTTGGCA CCCAGACCTA CATCTGCAAC GTGAATCACA AGCCCAAGCA CACCAAGGTC  
 TGAGATGAGG GAGTCGTGC ACCACTGGCA CGGGAGGTG TCGAACCCGT GGGTCTGGAT GTAGACGTTG CACTTAGTGT TCGGGTCTGT GTGGTTCCAG  
 181 L Y S L S S V V T V P S S S L G T Q T Y I C N V N H K P S N T K V  
 2001 GACAAGAAAG TTGAGCCCAA ATCTTGTGAC AAAACTCACC TCTAGAGTGG CGGTGGCTCT GGTCCGGTG ATGCTCGGT GCCGCGGGC GTTTTTTATG  
 CTGTTCTTTC AACTCGGTT TGAACACTG TTTTGAFTGG AGATCTCACC GCCACCGAGA CCAAGGCCAC TAGAGCCAA CGGCGGCCCG CAAAAATAC  
 214 D K K V E P K S C D K T H L O  
 2101 CTAGGCGCG CCTATACCTT GTCTGCCTCC CCGCGTTGCG TCGCGGTGCA TGGAGCCGG CCACCTCGAC CTGAATGGA GCGGCGGCA CCTCGGTAAC  
 GATCGCGCG GGATATGGA CAGACGGAG GCGCAACGC AGCGCCACGT ACCTCGGCC ACCTGAGCTG GACTTACCTT CCGCGGCCGT GGAGCGATTG

FIG. 32C

2201 GGATTCACCA CTCCAAGAAT TGGAGCCAAT CAATTCCTGC GGAGAACTGT GAATGCGCAA ACCAACCCCTT GGCAGAACAT ATCCATCGCG TCCGCCATCT  
 CCTAAGTGGT GAGGTCTCTA ACCTCGGTTA GTTAAGAAGC CCTCTTGACA CTACCGCGTT TGGTTGGAA CCGTCTTGTA TAGGTAGCGC AGCGGGTAGA  
  
 2301 CCAGCAGCCG CACGCGGCGC ATCTCGGGCA GCGTTGGGTC CTGGCCACGG GTGCGCATGA TCGTGCTCCT GTCGTTGAGG ACCCGGCTAG GCTGGCGGGG  
 GGTCTCGGC GTGCGCGCGG TAGAGCCCGT CGCAACCCAG GACCGGTGCC CACGGTACT AGCAGAGGA CAGCAACTCC TGGGCGGATC CGACCGCCOC  
  
 2401 TTGCGCTTACT GGTTAGCAGA ATGAATCACC GATACGCGAG CGAAGCTGAA GCGACTGCTG CTGCAAAAACG TCTGCGACCT GAGCAACAAC ATGAATGGTC  
 AACGGAATGA CCAATCGTCT TACTTAGTGG CTATGCGCTC GCTTGCACTT CGCTGACGAC GACGTTTTCG AGACGCTGGA CTCGTGTGTTG TACTTACCAG  
  
 2501 TTCGGTTTCC GTGTTTCGTA AAGTCTGGAA ACGCGGAAGT CAGCGCCCTG CACCATTTATG TTCCGGATCT GCATCGCAGG ATGCTGCTGG CTACCCCTGTG  
 AAGCCAAAGG CACAAGCAT TTCAGACCTT TCGCGCTTCA GTGCGGGAC GTGGTAATAC AAGCCCTAGA CGTAGCGTCC TAGCAGGACC GATGGGACAC  
  
 2601 GAACACCTAC ATCTGTATTA ACGAAGCGCT GGCATTGACC CTGAGTGATT TTCTCTCTGGT CCGCGCGCAT CCATACCGCC AGTTGTTTAC CCTCACAACG  
 CTTGTGGATG TAGACATAAT TGCTTCGCGA CCGTAAGTGG GACTCACTAA AAAGAGACCA GGGCGGGCGTA GGTATGGCGG TCAACAATA GGGTGTGTG  
  
 2701 TTCCAGTAAC CGGGCATGTT CATCATCAGT AACCCGTATC GTGAGCATCC TCCTCTCGTTT CATCGGATC ATTACCCCCA TGAACAGAAA TTCCCCCTTA  
 AAGTCAATG GCCCGTACAA GTAGTAGTCA TTGGGCATAG CACTCGTAGG AGAGAGCAAA GTAGCCATAG TAATGGGGGT ACTTGCTCTT AAGGGGAAT  
  
 2801 CACGGAGGCA TCAAGTGACC AAACAGGAAA AAACCGCCCT TAACATGGCC CGCTTTATCA GAAGCCAGAC ATTAACCGCTT CTGGAGAAAC TCAACGAGCT  
 GTGCCCTCCGT AGTTCACCTG TTTGTCTCTT TTTGGCGGGA ATGTACCGG GCGAATAAGT CTTCGGTCTG TAATGCGAA GACCTCTTTG AGTTGCTCGA  
  
 2901 GGACGCGGAT GAACAGGCAG ACATCTCTGA ATCGCTTCAC GACCACGCTG ATGAGCTTTA CCGCAGGATC CGGAAATGT AAACGTTAAT ATTTGTGTAA  
 CCTGGCGCTA CTTGTCCGTC TGTAGACACT TAGCGAAGTG CTGGTGGAC TACTCGAAT TACTCGAAT GCCTTTAA GCTTTTAA TAAACAAT  
  
 3001 AATTCGCGTT AAATTTTGT TAAATCAGCT CATTTTAA CCAATAGGCC GAAATCGGCA AAATCCCTTA TAAATCAAAA GAATAGACCG AGATAGGGTT  
 TTAAGCGCAA TTTAAAAACA ATTTAGTCGA GTAAAAAAT GGTATCCGG CTTTAGCCGT TTTAGGGAAT ATTTAGTTTT CTTATCTGGC TCTATCCCAA  
  
 3101 GAGTGTGTT CCAGTTTGA ACAAGAGTCC ACTATTAAAG AACGTGGACT CCAACGTCAA AGGGCGAAA ACCGTCTATC AGGGCTATGG CCCACTAGT  
 CTCACAACAA GGTCAAACCT TGTCTCAGG TGATAATTC TTGCACCTGA GGTTCAGTT TCCCGCTTTT TGGCAGATAG TCCCGATACC GGGTGTATGA

FIG. 32D

3201 GAACCAATCAC CCTAATCAAG TTTTTTGGGG TCGAGGTGCC GTAAAGCACT AAATCGGAAC CCTAAAGGGA GCCCCCGATT TAGAGCTTGA CGGGGAAAGC  
 CTGTGGTAGTG GGATTAGTTC AAAAAACCC AGCTCCACGG CATTTCTGTA TTAGACCTTG GGATTTCCCT CGGGGGCTAA ATCTCGAACT GCCCCTTTTCG  
  
 3301 CGGCGAAGCT GCGGAGAAAG GAAGGGAAGA AAGCGAAGG AGCGGGCGCT AGGGCGCTGG CAAGTGTAGC GGTACAGCTG CGCGTAACCA CCACACCCCG  
 GCCGCTTGCA CCGCTCTTTC CTTCCCTTCT TTTCCCTTCT TCCGCCGCTTCC TCGCCCGCGA TCCCGGACG GTTCACATCG CCAGTGGAC GCGCATTTGT GGTGTGGCG  
  
 3401 CGCGCTTAAT GCGCCGCTAC AGGGCGCTC CGATCTCTGC CTGCGCGCTT TCGGTGATGA CCGTGAAAC CTCTGACACA TGCAGCTCCC GGAGACGCTC  
 GCGCGAATTA CCGGCGGATG TCCCGGCGAG GCCTAGGACG GAGCGCGCAA AGCCACTACT GCCACTTTTG GAGACTGTGT ACCTCGAGGG CCTCTGCCAG  
  
 3501 ACAGCTTGTG TGTAAGCGGA TGCCGGGAGC AGACAAGCCC GTCAGGGGCG GTCAGCGGGT GTTGGCGGGT GTCGGGGCGC AGCATGACC CAGTCACGTA  
 TGTGGAACAG ACATTGCGCT ACGGCCCTCG TCTGTTCGGG CAGTCCCGG CAGTCGCCCA CAACCGCCCA CAGCCCCGG TCGGTACTGG GTCAGTGCAT  
  
 3601 GCGATAGCGG AGTGATATACT GGCTTAAC TA TCGGGCATCA GAGCAGATTG TACTGAGAGT GCACCATATG CCGTGTGAAA TACCGCACAG ATGCGTAAGG  
 CGCTATCGCC TCACATATGA CCGAATTGAT ACGCCGTAGT CTGCTCTAAC ATGACTCTCA CGTGGTATAC GCCACACTTT ATGGCGGTGC TACGCATTC  
  
 3701 AGAAATACC GCATCAGGG CTCTTCCGT TCCTCGCTCA CTGACTCGT GCGTCCGGT GGTCCGGTGC GCGAGCGGT ATCAGCTCAC TCAAAGGCGG  
 TCTTTTATGG CGTAGTCCG GAGAAGCGA AGGAGCGAGT GACTGAGCGA CCGAGGCCAG CAAGCCGACG CCGCTCGCCA TAGTCGAGTG AGTTTCCGCC  
  
 3801 TAATACGGTT ATCCACAGAA TCAGGGGATA ACGCAGGAAA GAACATGTGA GCAAAAGGCC AGCAAAAGCT AAAAAAGCG CGTTGCTGGC  
 ATTATGCCAA TAGGTGTCTT AGTCCCTAT TCGCTTCCGT CTGTGACTCT TCGTTTCCG GTCCTTGGCA TTTTTCGGC GCAACGACCG  
  
 3901 GTTTTTCAT AGGCTCCGCC CCGCTGACGA GCATCACA AAATCGACGT CAAGTCAGAG GTGGCGAAAC CCGACAGGAC TATAAAGATA CCAGGCGTTT  
 CAAAAGGTA TCCGAGGCG GGGGACTGCT CGTAGTCTTT TTAGCTGCGA GTTCAGTCTC CACCGCTTTG GGTGTCTTG ATATTCTAT GGTCCGCAAA  
  
 4001 CCCCCTGGAA GCTCCCTCGT CCGCTCTCTT GTTCGACCC TCGCGCTTAC CGGATACCTG TCCGCCCTTC TCCCTTCGG AAGCGTGGC CTTTCTCATA  
 GGGGGACCTT CGAGGGAGCA CCGGAGAGA CAAGCTGGG ACGGCGAATG GCCTATGGAC AGGCGGAAAG AGGGAAGCCC TTTCGACCCG GAAAGAGTAT  
  
 4101 GTCACGCTG TAGGTATCTC AGTTCCGGTG AGTTCGGTTC CTCCAGCTG GGTGTGTGTC ACGAACCCTC CGTTCAGCCC GACCGCTGCG CCTTATCCGG  
 CGAGTGGAC ATCCATAGAG TCAAGCCACA TCCAGCAAGC GAGTTCGAC CCGACACAG TGCTTGGGG GCAAGTCCGG CTGGCGACCG GGAATAGGCC  
  
 4201 TAACTATCGT CTTGATGCCA ACCCGGTAAG ACACGACTTA TCGGCACTGG CAGCAGCCAC TGGTAACAGG ATTAGCAGAG CGAGGTATGT AGCGGTGCT  
 ATTGATAGCA GAATCAGGT TGGGCCATTC TGTGCTGAAT AGCGTGACC GTCTCGGTG ACCATTGTCC TAATCGTCTC GCTCCATACA TCCGCCACGA

FIG. 3a



4301 ACAGAGTTCT TGAAGTGGTG GCCTAACTAC GGCTACACTA GAAGGACAGT ATTGGTATC TCGCTCTGC TGAAGCCAGT TACCTTCGGA AAAAGAGTTG  
 TGTCTCAAGA ACTTCACAC CGGATTGAT CCGATTGAT CTTCTGTCA TAAACCATAG ACGGAGAGC ACTTCGGTCA ATGGAAGCCT TTTTCTCAAC  
 4401 GTAGCTCTTG ATCCGGCAAA CAAACCACCG CTGGTAGCGG TGGTTTTTTT GTTTGCAAGC AGCAGATTAC GCGCAGAAAA AAAGGATCTC AAGAAGATCC  
 CATCGAGAAC TAGGCGGTTT GTTTGGTGGC GACCATCGCC ACCAAAAAAA CAAACGTCG TCGTCTAATG CCGGTCITTT TTTCTCTAGG TTCTTCTAGG  
 4501 TTTGATCTTT TCTACGGGT CTGACGCTCA GTGGAACGAA AACTCACGTT AAGGATTTT GGTCTAGAGA TTATCAAAAA GGATCTTCAC CTAGATCCTT  
 AAAC TAGAAA AGATGCCCCA GACTGCGAGT CACCTTGCTT TTGAGTGCAA TTCCCTAAAA CCAGTACTCT AATAGTTTTT CCTAGAAGTG GATCTAGGAA  
 4601 TTAATATAA AATGAAGTTT TAAATCAATC TAAAGTATAT ATGAGTAAAC TTGGTCTGAC AGTTACCAAT GCTTAATCAG TGAGGCACCT ATCTCAGCGA  
 AATTATAATT TTACTTCAAA ATTTAGTTAG ATTTCAATATA TACTCATTTG AACAGACTG TCAATGGTTA CGAATTAGTC ACTCCGTGGA TAGAGTCGCT  
 4701 TCTGTCTATT TCGTTCATCC ATAGTTGCCT GACTCCCGCT CGTGTAGATA ACTACGATAC GGGAGGGCTT ACCATCTGGC CCCAGTGTG CAATGATACC  
 AGACAGATAA AGCAAGTAGG TATCAACGGA CTGAGGGGCA GCACATCTAT TGATGCTATG CCTCCCGAA TGCTAGACCG GGTTCACGAC GTTACTATGG  
 4801 GCGAGACCCA CGCTCACCGG CTCCAGATT TFCAGCAATA AACAGCCAG CCGGAAGGC CGAGCGCAGA AGTGGTCTCG CACTTTATC CGCTCCATC  
 CGCTCTGGGT GCGAGTGGCC GAGGTCTAAA TAGTCTGTTAT TTGGTCTGCT GGCCTTCCCG GCTCGGCTCT TCACCAGGAC GTTGAATAAG GCGGAGGTAG  
 4901 CAGTCTATTA ATTGTTGCGG GGAAGCTAGA GTAAGTAGTT CGCCAGTTAA TAGTTTGGC AACGTTGTTG CCATTGCTGC AGGCATCGTG GTGTCACGCT  
 GTCAGATAAT TAACAACGGC CCTTCGATCT CATTCATCAA GCGGTCAATT ATCAAAACGG TTGCAACAAC GGTAAACGACG TCCGTAGCAC CACAGTGCGA  
 5001 CGTCTGTTGG TATGGCTTCA TTCAGCTCCG GTTCCCAACG ATCAAGGCGA GTTACATGAT CCCCCATGTT GTGCAAAAAA GCGGTAGCT CTTCTGGTCC  
 GCAGCAAACC ATACCGAAGT AAGTCGAGG CAAGGGTTGC TAGTTCCGCT CAATGTAATA GGGGTACAA CACGTTTTTT CGCCAATCGA GGAAGCCAGG  
 5101 TCCGATCGTT GTCAGAAATA AGTTGGCCGC AGTGTTATCA CTCATGGTTA TGGCAGCACT GCATTAATCT CTTACTGTCA TGCCATCCGT AAGATGCTTT  
 AGGCTAGCAA CAGTCTTCAT TCAACCGGCG TCACAATAGT GAGTACCAAT ACCGTCGTGA CGTATTAGA GAATGACAGT ACGGTAGGCA TTCTACGAAA  
 5201 TCTGTGACTG GTGAGTACTC AACCAAGTCA TTCTGAGAAAT AGTGATGCG GCGACCGAGT TGCTTTGCC CGGGGTCAAC ACGGATAAT ACCGCGCCAC  
 AGACACTGAC CACTCATGAG TTGGTTTCAGT AAGACTCTTA TCACATACGC CGCTGGCTCA ACGAGAACGG GCCGAGTTG TGCCCTATTA TGGCGCGGTG

FIG. 32F



5301 ATAGCAGAAC TTATAAAGTG CTCATCAFTG GAAAACGTTT TCGGGGGCGA AAACCTCTCAA GGATCTTACC GCTGTTGAGA TCCAGTTTGA TGTAACCCAC  
 TATCGTCTTG AAATTTTCAC GAGTAGTAAC CTTTGTGCAAG AAGCCCCGCT TTTGAGAGTT CCTAGAATGG CGACAATCT AGGTCAAGCT ACATTGGGTG  
 5401 TCGTGCACCC AACTGATCTT CAGCATCTTT TACTTTTACC AGCGTTTCTG GGTGAGCAAA AACAGGAAGG CAAAAAGCG CAAAAAGGG AATAAGGGCG  
 AGCACGTGGG TTGACTAGAA GTCGTAGAAA ATGAAAGTGG TCGCAAGAC CCACTCGTTT TTGTCCTTCC GTTTTACGGC GTTTTTCCTC TTATTCCCGC  
 5501 ACACGGAAAT GTTGAATACT CATACTCTTC CTTTTTCAAT ATTATTGAAG CATTATATCAG GGTATATGTC TCATGAGCGG ATACATATTT GAATGTATTT  
 TGTGCCCTTA CAACCTATGA GTATGAGAAG GAAAAAGTGA TAATAACTTC GTAAATAGTC CCAATAACAG AGTACTCGCC TATGTATAAA CTTACATAAA  
 5601 AGAAAAATAA ACAATAGGG GTTCCGGCGA CATTTCCCGG AAAAGTGCCA CCTGACGTCT AAGAAACCAT TATTATCATG ACATTAACCT ATAAAAATAG  
 TCTTTTTTATT TGTATTATCC TGTTTATCCC CAAGGCGCGT GTAAAGGGGC TTTTACCGGT GGAATGCAGA TTCTTTGGTA ATAAATAGTAC TGTAAATGGA TATTTTATC  
 5701 GCGTATCAG AGGCCCTTTC GTCTTCAATA CAGGTAGACC TTTTCGTAGAG ATGTACAGTG AATCCCGGA AATATACAC ATGACTGAAG GAAGGGAGCT  
 CGCATAGTGC TCCGGGAAAG CAGAAATAT GTCCATCTGG AAGCATCTC TACATGTAC TTTAGGGGCT TTAATATGTG TACTGACTTC CTTCCCTCGA  
 5801 CGTCATTCCC TGCCGGGGTTA CGTCACCTAA CATCACTGTT ACTTTAAAAA AGTTTCCACT TGACACTTTG ATCCCTGATG GAAAACGCAT AATCTGGGAC  
 GCAGTAAGGG ACGGCCCAAT GCAGTGGATT GTAGTACAAA TGAAATTTTT TCAAAGGTGA ACTGTGAAAC TAGGGACTAC CTTTTCGGTA TTAGACCCGTG  
 5901 AGTAGAAAGG GCTTCAATCAT ATCAAAATGCA ACGTACAAAG AAATAGGCGT TCTGACCTGT GAAGCAACAG TCAATGGGCA TTTGTATAAG ACAAACTATC  
 TCATCTTTCC CGAAGTAGTA TAGTTTACGT TGTATCCCGA AGACTGGACA CTTTGGTGTG AGTTACCCGT AAACATATTC TGTGTGATAG  
 6001 TCACACATCG ACAAAACCAAT ACAATACAGG TAGACCTTTC GTAGAGATGT ACAGTGAAT CCCCAGAAAT ATACACATGA CTGAAGGAAG GGAGCTCGTC  
 AGTGTGTAGC TGTTTGGTTA TGTATGTCC ATCTGGAAAG CATCTCTACA TGTCACTTTA GGGGCTTTAA TATGTGTACT GACTTCTTTC CCTCGAGCAG  
 6101 ATTCCCTGCC GGGTTAGTGC ACCTAACATC ACTGTTACTT TAAAAAGTT TCCACTTGAC ACTTTGATCC CTGATGGAAA ACGCATATC TGGGACAGTA  
 TAAGGGACGG CCCAATGCAG TGGATTGTAG TGACAATGAA ATTTTTTCAA AGGTGAACTG TGAACCTAGG GACTACCTTT TCGGTATTAG ACCCTGTCTAT  
 6201 GAAAGGGCTT CATCATATCA AATGCAACGT ACAAGAAAT AGGCTTCTG ACCCTGGAAG CAACAGTCAA TGGGCATTTG TATAAGACAA ACTATCTCAC  
 CTTTCCCGAA GTAGTATAGT TTACGTTGCA TGTCTCTTTA TCCCGAAGAC TGGACACTTC GTTGTCTAGT ACCCGTAAAC ATATTCTGTT TGATAGAGTG  
 6301 ACATCGACAA ACCAATACAA TCTACAGGTA GACCTTTCGT AGAGATGTAC AGTGAATCC CCGAAATAT ACACATGACT GAAGGAAGGG AGCTCGTCTAT  
 TGTAGCTGTT TGGTTATGTT AGATGTCCAT CTGGAAGCA TCTCTACATG TCACCTTAGG GGCCTTAATA TGTGTACTGA CTTCTCTTCC TCGAGCAGTA  
 6401 TCCCTGCCGG GTTACGTCAC CTAACATCAC TGTACTTTA AAAAGTTTC CACTTGACAC TTTGATCCCT GATGGAAGC GCATAATCTG GGACAGTAGA  
 AGGGACGGCC CAATGCAGTG GATTGTAGTG ACAATGAAAT TTTTTCAAAG GTGAACGTGT AACTTAGGGA CTACCTTTTG CGTATTAGAC CCTGTCTCT  
 6501 AAGGGCTTCA TCATATCAAA TGCAAGGTAC AAAGAAATAG GGCTTCTGAC CTGTGAAGCA ACAGTCAATG GGCATTTGTA TAAGACAAAC TATCTCACAC  
 TTCCCGAAGT AGTATAGTTT ACGTTGCATG TTTCTTTTATC CCGAAGACTG GACACTTCTG TGTCAAGTAC CCGTAAACAT ATTCTGTGTTG ATAGAGTGTG  
 6601 ATCGACAAAC CAATACAATC  
 TAGCTGTTTG GTTATGTTAG

FIG. 326

1 TTCGAGCTCG CCCGACATTG ATTATTGACT AGTTATTAAAT TACGGGGTCA TTAGTTTATA GCCCATATAT GGAGTCCGC GTTACATAAC  
AAGCTCGAGC GGGCTGTAAC TAATAACTGA TCAATAATTA ATGCCCCAGT AATCAAGTAT CCGGTATATA CCTCAAGGCG CAATGTATTG  
101 TTACGGTAAA TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCCATG ACGTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA  
AATGCCATTT ACCGGGCGGA CCGACTGGCG GGTGCTGGG GGGGGTAAAC TGCAGTTATT ACTGCATACA AGGTATCAT TCGGTTATC OCTGAAAGGT  
201 TTGACGTCAA TGGGTGGAGT ATTTACGGTA AACTGCCAC TTGGCAGTAC ATCAAGTGA TCATATGCCA AGTACGCCCT CTATTGACGT CAATGACGGT  
AACTGCAGTT ACCCACCCTCA TAAATGCCAT TTGACGGGTG AACCGTCATG TAGTTCACAT AGTATACGGT TCATGCGGGG GATAACTGCA GTTACTGCCA  
301 AAATGGCCCG CCTGGCATTA TGCCCAGTAC ATGACCTTAT GGGACTTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC ATGGTGATGC  
TTTACCGGGC GGACCGTAAT ACGGTCATG TACTGGAATA CCTGAAAGG ATGAACCGTC ATGTAGATGC ATAAATCAGTA GCGATPAAATGG TACCACCTAGC  
401 GGTTTTGGCA GTACATCAAT GGGCGTGGAT AGCGGTTTGA CTCACGGGA TTTCCAAGTC TCCACCCCAT TGACGTCAT GGGAGTTTGT TTTGGCACCA  
CCAAAACCGT CATGTAGTTA CCCGCACCTA TCGCCAAACT GAGTGCCCCCT AAAGTTTACG AGTGGGGTA ACTGCAGTTA CCTCAACA AAACCGTGGT  
501 AAATCAACGG GACTTTCCAA AATGTCGTAA CAACTCCGCC CCATTGACG AATGGGCGG TAGCGTGTA CCGTGGGAGG TCTATATAAG CAGAGCTCGT  
TTTAGTTGCC CTGAAAGGTT TTACAGCATT GTTGAGCGG GGTAACTGG TTTACCCGCC ATCCGCACAT GGCACCCCTCC AGATATATTC GTCTCGAGCA  
601 TTAGTGAACC GTCAGATCGC CTGGAGACGC CATCCACGCT GTTTTGACCT CCATAGAAGA CACCGGGACC GATCCAGCCT CCGCGGCCCG GAACGCTGCA  
AATCACTTGG CAGTCTAGCG GACCTCTGG GAGGTGCGA CAAAACCTGA GGTATCTTCT GTGGCCCTGG CTAGGTCCGA GCGCGCCGCC CTTGCCACGT  
701 TTGGAACGGG GATTCGCCCT GCCAAGAGTG ACGTAAGTAC CGCCTATAGA GTCTATAGG CACCCCTT GGCITCGTTA GAACGCGGCT ACAATTAATA  
AACCTTGGCG CTAAGGGGCA CCGTTCTCAC TGCATTATG GCGGATATCT CAGATATCCG GGTGGGGGAA CCGAAGCAAT CTTGCGCCGA TGTAAATAT  
801 CATAACCTTA TGTATCATAC ACATACGATT TAGGTGACAC TATAGAATAA CATCCACTTT GCCTTTCTCT CCACAGGTGT CCACTCCOAG GTCCAACCTGC  
GTATTGGAAT ACATAGTATG TGTATGCTAA ATCCACTGTG ATATCTTATT GTAGTGAAA CCGAAAGAGA GGTGTCCACA GGTGAGGTC CAGGTTGACG  
901 ACCTCGGTC TATCGATTGA ATTCCACCAT GGGATGGTCA TGTATCATCC TTTTCTTAGT AGCAACTGCA ACTGGAGTAC ATTCAGATAT CCAGATGACC  
TGGAGCCAAAG ATAGCTAACT TAAGGTGCTA CCTTACCAGT ACATAGTAGG AAAAAGATCA TCGTTGACGT TGACCTCATG TAAGTCTATA GGTCTACTGG  
1 M G W S C I I L F L V A T A T G V H S D I Q M T  
^met ^Start VL ^EcoRV

FIG. 33 A

1001 CAGTCCCCGA GTCCTCTGTG CGCCTCTGTC TCACCATCAC CTGCGTGCC AGTCAGGATG TGTCCACTGC TGTAGCCTGG TATCAACAGA  
 GTCAGGGGCT CGAGGACAC CGCTATCCC AGTGGTAGT GACGGACGG TCAGTCTTAC ACAGGTGAG ACATCGGACC ATAGTTGTCT  
 25 Q S P S S L S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K  
 ^CDR-L1  
 1101 AACCAGGAAA AGCTCCGAG CTTCTGATTT ACTCGGCATC CTTCCTCTAC TCTGGAGTCC CTTCTCGCTT CTCTGTAGC GGTTCGGGA CGGATTTTCAC  
 TTGGTCCCTTT TCGAGGCTTC GAAGACTAAA TGAGCCGTAG GAAGGAGATG AGACCTCAGG GAAGACGAA GAGACCATCG CCAAGGCCCT GCCTAAAGTG  
 59 P G K A P K A P K L L I Y S A S F L Y S G V P S R F S G S G S G T D F T  
 ^CDR-L2  
 1201 TCTGACCATC AGCAGTCTGC AGCCGGAAGA CTTCCGCAACT TATTACTGTC AGCAATCTTA TACTACTCCT CCACGTTTCG GACAGGTAC CAAGGTGGAG  
 AGACTGGTAG TCGTCAGACG TCGGCCCTCT GAAGCCTTGA ATAATGACAG TCGTTAGAAT ATGATGAGGA GGTGCAAGC CTGTCCCATG GTTCCACCTC  
 92 L T I S S L Q P E D F A T Y Y C Q Q S Y T T P P T F G Q G T K V E  
 ^CDR-L3  
 1301 ATCAAACGAA CTGTGGCTGC ACCATCTGTC TTCACTCTCC CGCCATCTGA TGAGCAGTTG AAATCTGGAA CTGCTTCTGT TGTGTGCTTG CTGAATAACT  
 TAGTTTGCTT GACACCGACG TGGTAGACAG AAGTAAAGG GCGGTAGACT ACTCGTCAAC TTTAGACCTT GACGAAGACA ACACACGGAC GACTTATTTGA  
 125 I K R T V A A P S V F I F P P S D E Q L K S G T A S V V C L L N N F  
 ^start human kappa  
 401 TCTATCCCAG AGAGGCAAA GTACAGTGA AGGTGGATA CGCCTCCAA TCGGGTAAT CCCAGGAGAG TGTACACAG CAGGACAGCA AGGACAGCAC  
 AGATAGGGTC TCTCCGGTTT CATGTCACCT TCCACCTATT GCGGAGGTT AGCCCATTTA GGTCTCTC ACAGTGTCTC GTCTGTCTGT TCCTGTCTGT  
 159 Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T  
 501 CTACAGCCTC AGCAGCACCC TGACGCTGAG CAAAGCAGAC TAGGAGAAAC ACAAGTCTA CGCCTGGAA GTCACCCATC AGGGCCTGAG CTCGCCCGTC  
 GATGTCGGAG TCGTCGTGG ACTGCGACTC GTTTCGTCTG ATGCTCTTTG TGTTCAGAT GCGGACGCTT CAGTGGGTAG TCCCGGACTC GAGCGGGCAG  
 192 Y S L S S T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V  
 601 ACAAGAGCT TCAACAGGGG AGAGTGTAA GCTTGGCCCG CATGGCCCAA CTGTGTTATT GCAGTTATA ATGTTTACAA ATAAAGCAAT AGCATCACAA  
 TGTCTCTCGA AGTTGTCCCC TCTCACAATT CGAACCGGCG GTACCGGGT GAACAAATAA CGTCGAATAT TACCAATGTT TATTTCGTTA TCGTAGTGTT  
 225 T K S F N R G E C O

FIG. 33b

1701 ATTTCACAAA TAAAGCATT TTTTCACTGC ATTCTAGTTG TGGTTTGTCC AAACATCATCA ATGTATCTTA TCATGTCTGG ATCGGGAATT AATTCCGGCGC  
 TAAAGTGTTT ATTTCCGTAA AAAAGTGACG TAAGATCAAC ACCAAACAGG TTTGAGTAGT TACATAGAAT AGTACAGACC TAGCCCTTAA TTAAAGCCGCG  
 1801 AGCACCATGG CCTGAAATAA CCTCTGAAAG AGGAACCTGG TTAGGTATCT TCTGAGGGCG AAAGAACCAG CTGTGGAATG TGTGTCACTT AGGGTGTGGA  
 TCCGTGGTACC GGACTTTATT GGAGACTTTC TCCTTGAACC AATCCATAGA AGACTCCGCC TTTCTTGGTC GACACCTTAC ACACAGTCAA TCCCACACCT  
 ^change from C to T, kill KpnI site  
 1901 AAGTCCCCAG GCTCCCCAGC AGGCAGAAAT ATGCAAAGCA TGCATCTCAA TTAGTCAGCA ACCAGGTGTG GAAAGTCCCC AGGTCCCCA GCAGGCAGAA  
 TTCAGGGGTC CGAGGGGTG TCCGTCCTCA TACGTTTCGT ACCTAGAGTT AATCAGTCGT TGGTCCACAC CTTTCAGGGG TCCGAGGSET CGTCCGTCIT  
 2001 GTATGCAAAG CATGCATCTC AATTAGTCAG CAACCATAGT CCGCCCCCTA ACTCCGCCCA TCCCGGCCCT AACTCCGCC AGTCCGCC ATTCCTCCGC  
 CATACGTTTC GTACGTAGAG TTAATCAGTC GTTGGTATCA GGGCGGGGT TGAGGGGGG TTAGGGCGG TCAAGGGCGG TAAGAGGGCG  
 2101 CCATGGCTGA CTAATTTTTT TTATTTATGC AGAGGCCGAG GCGCCCTCG CCTCTGAGCT ATTCAGAAAG TAGTGAGGAG GCITTTTTTGG AGGCCTAGGC  
 GGTACCGACT GATTAAAAA AATAAATAGG TCTCCGGCTC GGGCGGAGCC GGAGACTCGA TAAGTCTTC ATCACTCTC CGAAAAAAC TCCGGATCCG  
 2201 TTTTGC AAAA AGCTGTAAAC AGCTTGGCAC TGGCCGTCGT TTTACAACGT CGTACTGGG AAAACCTCG CGTAPCCAA CTTAATCGCC TTGCAGCACA  
 AAAACGTTTT TCGACAATTG TCGAACCGTG ACCGGCAGCA AATGTTGCA GCACTGACCC TTTTGGGACC GCAATGGGT GAATTAGCG AACGTCTGT  
 2301 TCCCCCCTC GCCAGCTGGC GTAATAGCGA AGAGGCCCGC ACCGATCGCC CTTCCCAACA GTTGCCTAGC CTGAATGGCG AATGGCGCCT GATGCCGTAT  
 AGGGGGGAG CGGTCCGACG CATTATCGCT TCTCCGGGCG TGGCTAGCG GAAGGTTGT CAACGCATCG GACTTACCG TTACCGCGGA CTACGCCATA  
 2401 TTTCTCCTTA CGCATCTGTG CGGTATTTCA CACCGCATAC GTCAAAGCAA CCATAGTACG CGCCCTGTAG CGCGCATTA AGCGGGCGG GTGTGTGGT  
 AAAGAGGAAT GCGTAGACAC GCCATAAAGT GTGGCGTATG CAGTTTCTGT GGTATCATGC GCGGGACATC GCCCGGTAAT TCGCGCCGCC CACACACCA  
 2501 TACGGCAGC GTGACCGCTA CACTTGCCAG CGCCCTAGCG CCGGCTCCTT TCGCTTCTCT CCCTTCTCTT CTCGCCACGT TCGCCGGCTT TCCCGGTCAA  
 ATGCGCGTCG CACTGGCGAT GTGAACGGTC GCGGATCGC GGGCGAGGAA AGCGAAAGAA GGAAGGAAA GAGCGGTGCA AGCGGCCGAA AGGGCAGTT  
 2601 GCTCTAATC GGGGGCTCCC TTTAGGGTTC CGATTATAGT CTTTACGGCA CCTCGACCCC AAAAACTTG ATTTGGGTGA TGGTTCACGT AGTGGGCCAT  
 CGAGATTAG CCCCCGAGG AATCCCAAG GCTAAATCAC GAAATGCCGT GGAGCTGGG TTTTGTGAAC TAAACCCACT ACCAAGTGCA TCACCCGGTA

56/75

FIG. 33 C

2701 CGCCCTGATA GACGGTTTTT CGCCCTTTGA CGTTGGAGTC CACGTTCTTT AATAGTGGAC TCTTGTTC AACTGGAACA AACTCAACC CTATCTCGG  
 GCGGACTAT CTGCCAAAA GCGGAACT GCAACCTCAG GTGCAAGAAA TTATCACCTG AGAACAGGT TTGACCTTGT TGTGAGTTGG GATAGAGCCC  
 2801 CTATTCTTTT GATTATTAAG GGATTTTGGC GATTTCGGCC TATTGTTAA AAAATGAGCT GATTTAACA AAAATTTAACG CGAATTTTAA CAAAATATTA  
 GATAAGAAAA CTAAATATTC CTTAAACCG CTAAAGCCCG ATAACCAATT TTTTACTCGA CTAATTTGTT TTTAAATTGC GCTTAAATTT GTTTTATAAT  
 2901 ACCTTTACAA TTTTATGGTG CACTCTCAGT ACAATCTGCT CTGATGCCG ATAGTTAAGC CAACTCCGCT ATCGCTACGT GACTGGGTCA TGGCTGCGCC  
 TGCAAATGTT AAAATACCAC GTGAGAGTCA TGTAGACGA GACTACGGCG TATCAATTCC GTTGAGGCGA TAGCGATGCA CTGACCCAGT ACCGACGCGG  
 3001 CCGACACCCG CCAACACCCG CTGACGGGCT TGTCTGCTCC CGGCATCCGC TTACAGACAA GCTGTGACCG TCTCCGGGAG CTGCATGTGT  
 GGCTGTGGG GGTGTGGG GACTGCGCG GACTGCCCGA ACAGACGAGG GCGTAGGCG AATGCTGTT CGACACTGGC AGAGGCCCTC GACGTACACA  
 3101 CAGAGGTTTT CACCGTCATC ACCGAAACG GCGAGGCAGT ATTCTTGAAG ACGAAAGGC CTCGTGATAC GCTATTTT ATAGGTTAAT GTCATGATAA  
 GTCTCCAAA GTGGCAGTAG TGGCTTTGCG CGCTCCGTC TAAGAACTTC TGTCTCCG GAGCACTATG CGGATAAAAA TATCCAATTA CAGTACTATT  
 3201 TAATGGTTT TTAGACGTCA GGTGGCACTT TTGCGGGA TGTGCGGGA ACCCTATTT GTTTATTTT CTAAATACAT TCAAAATATGT ATCCGCTCAT  
 ATTACCAAAG AATCTGCAGT CCACCGTGAA AAGCCCCCTT ACACGGCCT TGGGGATAAA CAAATAAAAA GATTTATGTA AGTTTATACA TAGGCGAGTA  
 3301 GAGACAAATA CCTGATAA TGCTTCAATA ATATTGAAA AGGAAGAGTA TGAGTATTCA ACATTTCCGT GTGCCCCCTT TCCCTTTTTT TCGCGCATTT  
 CTCGTGTTAT GGGACTATTT ACGAAGTTAT TATAACTTTT TCCTTCTCAT ACTCATAAGT TGTAAGGCA CAGCGGGAAT AAGGAAAAA ACGCGTAAA  
 3401 TGCCTTCTCTA CCGAGAAACG CTGGTGAAG TAAAGATGC TGAAGATCAG TTGGGTGCAC GAGTGGGTTA CATCGAACTG GATCTCAACA  
 ACGGAAGGAC AAAAACGAGT GGGTCTTTGC GACCACCTTC ATTTTCTACG ACTTCTAGTC AACCCACGTG CTCACCCAAT GTAGCTTGAC CTAGAGTTGT  
 3501 GCGGTAAGAT CCTTGAGAT TTTTCGCCCG AAGAAGTTT TCCAATGATG AGCATTTTA AGTTCTGCT ATGTGGCGG GTATTATCCC GTGATGACGC  
 CGCCATTCTA GGAACCTCA AAAGCGGGG TTCTTGCAA AGGTACTAC TCGTGAAAAT TTCAAGACGA TACACCGCGC CATAATAGG CACTACTGCG  
 3601 CCGGCAAGAG CAACTCGGTC GCCGCATACA CTATTCTCAG AATGACTGG TTGAGTACTC ACCAGTCACA GAAAAGCATC TTACGGATGG CATGACAGTA  
 CCCCCTTCTC GTTGAGCCAG CCGCGTATGT GATAAGAGTC TTAAGAACC AATCATGAG TGGTCAGTGT CTTTTCTGAG AATGCTTACC GTACTGTCTAT

57/75

FIG. 33 D

3701 AGAGAAATTAT GCAGTGCTGC CATAAACCATG AGTGATTAACA CTGCGGGCCAA CTTACTTCTG ACAACGATCG GAGGACCGAA GGAGCTAACCC GCCTTTTTCG  
 TCCTCTTAATA CGTCACGACG GTATTGGTAC TCACATATGT GACGCGGCTT GAATGAAGAC TGTGTCTAGC CTCCTGGCTT CCTCGATGG CGAAAAAAGC  
 3801 ACACATAGGG GGATCATGTA ACTCGCCTTG ACTCGTTGGG ACCGGAGCTG AATGAAGCCA TACCAAAACGA CGAGCGTGAC ACCACGATGC CAGCAGCAAT  
 TGTGTATACC CCTAGTACAT TGAGCGGAAC TAGCAACCCCT TGGCCTCGAC TTACTTCCGT ATGGTTTGCT GCTCGCACTG TGGTGCTACG GTCTCGTTA  
 3901 GGCAACAACG TTGCGGCAAC TATTAACCTG CGAACTACTT ACTCTAGCTT CCCGGCAACA ATTAATAGAC TGGATGGAG CGGATAAAGT TGCAGGACCA  
 CCGTTGTTGC AACGCGTTG ATAATTGACC GCTTGATGAA TGAGATCGAA GGGCCCTTGT TAATTATCTG ACCTACCTCC GCCTATTTC ACGTCTCTGT  
 4001 CTCTCTGGCT CGGCCCTTCC GGCTGGCTGG TTTATTGCTG ATAAATCTGG AGCGGTGAG CGTGGGTCTC GCGGTATCAT TGCAGCACTG GGGCCAGATG  
 GAAGACGCGA GCCGGGAAG CCGACCGACC AAATAACGAC TATTTAGACC TCGGCCACTC GCACCCAGAG CGCCATAGTA ACGTCTGTAC CCCGGTCTAC  
 4101 GTAAGCCCTC CCGTATCGTA GTTATCTACA CGACGGGGAG TCAGGCAACT ATGGATGAAC GAAATAGACA GATCGGTGAG ATAGGTGCTT CACTGATTAA  
 CATTCGGGAG GGCATAGCAT CAATAGATGT GCTGCCCTTC AGTCCGTTGA TACCTACTTG CTTTATCTGT CTAGGACTC TATCCACGGA GTGACTAATT  
 4201 GCATTGGTAA CTGTCAGACC AAGTTTACTC ATATATACTT TAGATTGATT TAAACCTTCA TTTTAAATTT AAAAGGATCT AGGTGAAGAT CCCTTTTGAT  
 CGTAACCAAT GACAGTCTGG TTCAAATGAG TATATATGAA ATCTAACTAA ATTTTGAAGT AAAAATTAAT TTTTCTAGA TCCACTTCTA GGAAAACTA  
 4301 AATCTCATGA CCAAAATCCC TTAACGTGAG TTTTCTGTTCC ACTGAGGCTC AGACCCCGTA GAAAGATCA AAGGATCTTC TTGAGATCCT TTTTCTCTGC  
 TTAGAGTACT GGTTTTAGGG AATTGCACCT AAAAGCAAGG TGACTCGCAG TCTGGGGCAT CTTTCTAGT TTCTTAGAAG AACTCTAGGA AAAAAGAGC  
 4401 GCGTAATCTG CTGCTTGCAA ACAAAAAAC CACCGCTACC AGCGGTGGTT TGTTCGCGG ATCAAGAGCT ACCAATCTT TTTCGGAAG TAACTGGCTT  
 CGCATTAGAC GACGAACGTT TGTTTTTTTG GTGGCGATGG TCGCCACCAA ACAACCGCC TAGTTCTCGA TGGTTGAGAA AAAGGCTTCC ATTGACCGAA  
 4501 CAGCAGAGCG CAGATACCAA ATACTGTCTT TCTAGTGTAG CCGTAGTTAG GCCACCACTT CAAGAATCTT GTAGCACCGC CTACATACCT CGCTCTGCTA  
 GTCGTCTCGC GTCTATGGTT TATGACAGGA AGATCACATC GGCATCAATC CGGTGGTGAA GTTCTTGAGA CATCTGGCG GATGTATGGA GCGAGACGAT  
 4601 ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC GATAAGTCTG GTCTTACCG GTTGGACTCA AGAGGATAGT TACCGGATAA GCGCGACGGG TCGGGCTGAA  
 TAGGACAAATG GTCACCGAGC ACGGTACCG CTATTTCAGCA CAGAATGGCC CAACCTGAGT TCTGCTATCA ATGGCTTATT CCGCGTGGCC AGCCCCGACTT

4701 CGGGGGGTTT GTGCACACAG CCCAGCTTGG AGCGAACGAC CTACACCGAA CTGAGATACC TACAGCGTGA GCATTGAGAA AGCGCCACGC TTCCCCGAAGG  
 GCCCCCAAG CACGTGTGTC GGGTCGAACC TCGCTTGCTG GATGTGGCTT GACTCTATGG ATGTCCCACT CGTAACTCTT TCGCGGTGCG AAGGGCTTCC  
  
 4801 GAGAAAGCG GACAGGTATC CGGTAAGCG CAGGGTCGGA ACAGGAGAGC GCACGAGGA GCTTCCAGGG GGAACGCCCT GGTATCTTTA TAGTCTGTGTC  
 CTCCTTCCGC CTGTCCATAG GCCATTTCGCC GTCCCAGCCT TGTCTCTCTG CGTGCTCCCT CGAAGGTCCC CCTTTGCGGA CCATAGAAAT ATCAGGACAG  
  
 4901 GGGTTTCGCC ACCCTGACT TGAGCGTCTGA TTTTGTGAT GCTCGTCAGG GGGGCGGAGC CTATGGAAAA ACGCCAGCAA CGCGGCCCTTT TTACGGTTCC  
 CCCAAAGCGG TGGAGACTGA ACTCGCAGCT AAAAACACTA CGAGCAGTCC CCCCGCTCG GATACCTTTT TCGGGTCGTT GCGCCGGA AATGCCAAGG  
  
 5001 TGGCCTTTTG CTGGCCTTTT GCTCACATGT TCTTTCCTGC GTTATCCCCT GATTCTGTGG ATAACCGTAT TACCGCCCTTT GAGTGAGCTG ATACCGCTCG  
 ACCGGAAAA GACCGGAAAA CGAGTGTACA AGAAGGACG CAATAGGGA CTAAGACACC TATTGGCATA ATGGCGGAAA CTCACCTCGAC TATGGCGAGC  
  
 5101 CCGCAGCCGA ACGACCGAGC GCAGCGAGTC AGTGAGCGAG GAAGCGGAAG AGCGCCCAAT ACGCAAACCG CCTCTCCCG CGCGTTGGCC GATTCATTAA  
 GGCGTCGGCT TGCTGGCTCG CGTGGCTCAG TCACCTCGCTC CTTCGCCCTTC TCGCGGTTA TCGGTTGGC GGAGAGGGGC GCGCAACCG CTAAGTAATT  
  
 5201 TCCAGCTGGC ACGACAGGTT TCCCGACTGG AAAGCGGCA GTGAGCGCAA CGCAATTAA GTGAGTTACC TCACCTCATTA GGCACCCCG GCTTTTACACT  
 AGGTCCACCG TGCTGTCCAA AGGGCTGACC TTTCGCCCCG CACTCGCGTT GCGTTAATTA CACTCAATGG AGTGAGTAAT CCGTGGGGTC CGAAATGTGA  
  
 5301 TTATGCTTCC GGCTCGTATG TTGTGTGGA TTGTGAGCGG ATAACAATTT CACACAGGA ACAGCTATGA CCATGATTAC GAATTAA  
 AATACGAAG CCGAGCATAC AACACACCTT AACACTCGCC TATTGTAAA GTGTGTCCCT TGTGATACT GGTACTAATG CTTAATT

FIG. 33F



```

1  ATTCCGAGCTC GCCCGACATT GATTATTGAC TAGTTATTAA TAGTAATCAA TTACGGGGTC ATTAGTTTCAT AGCCCATATA TGGAGTCCG CGTTACATAA
   TAAGCTCGAG CGGGCTGTAA CTAATAACTG ATCAATAATT ATCAATTAGTT AATGCCCCAG TAATCAAGTA TCGGGTATAT ACCTCAAGGC GCAATGTATT

101 CTTACGGTAA ATGGCCCGCC TGGCTGACCG CCCAAGCACC CCCGCCCATT GACGTCAATA ATGACGATAG TTCCCATAGT AACGCCAATA GGGACTTTCC
   GAATGCCATT TACCGGGCGG ACCGACTGGC GGGTTGCTGG GGGGGGTAA CTGCAGTTAT TACTGCATAC AAGGGTATCA TTGCGGTTAT CCTGAAAGG

201 ATTGACGTCA ATGGGTGGAG TATTTACGCT AAACGCCCCA CTGGGCAGTA CATCAAGTGT ATCAATAGCC AAGTACGGCC CCTATTGACG TCAATGACGG
   TAACTGCAGT TACCCACCTC ATAAATGCCA TTTGACGGGT GAACCGTTCAT GTAGTTCACA TAGTATACGG TTCAATGCGG GGATAACTGC AGTTACTGCC

301 TAAATGGCCC GCGTGGCATT ATGCCCAGTA CATGACCTTA TGGGACTTTC CTACTTGGCA GTACATCTAC GTATTAGTCA TCGCTATTAC CATGGTGATG
   ATTTACCGGG CGGACCGTAA TACGGGTTCAT GTACTGGAAT ACCCTGAAAG GATGAACCGT CATGTAGATG CATTAATCAGT AGCGATAATG GTACCCACTAC

401 CGGTTTGGC AGTACATCAA TGGGCGTGGG TAGCGGTTTG ACTCAGCGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAA TGGGAGTTTG TTTTGGCACC
   GCCAAAACCG TCATGTAGTT ACCCGCACCT ATCGCCAAAC TGAGTGCCCC TAAAGTTCA GAGGTGGGT AACTGCAGTT ACCCTCAAAC AAAACCGTGG

501 AAAATCAACG GGACTTTCCA AAATGTCGTA ACAACTCCGC CCCATTGAGC CAAATGGGCG GTAGGCGTGT ACGGTGGGAG GTCTATATAA GCAGAGCTCG
   TTTTACTTGC CCTGAAAGGT TTTACAGCAT TGTTCAGGCG GGGTAACATC GTTTACCCGC CATCCGCACA TGCACCCCTC CAGATATATT CGTCTCGAGC

601 TTTAGTGAAC CGTCAGATCG CCTGGAGAGC CCATCCACGC TGTTTTGACC TCCATAGAG ACACCGGGAC CGATCCAGCC TCCGGGGCGG GGAACGGTGC
   AAATCACTTG GCAGTCTAGC GGACCTCTGC GGTAGGTGCG ACAAACTGG AGGTATCTTC TGTGGCCCTG GCTAGGTGCG AGGCGCCGCG CCTTGCCACG

701 ATTGGAACGC GGATTCCCCG TGCCAAGAGT GACGTAAGTA CCGCTATAG AGTCTATAGG CCCACCCCTT TGGCTTCGTT AGAACGCGGC TACAATTAAT
   TAACCTTGC CCAAGGGC ACGGTTCTCA CTGCATTTCAT GCGGATATC TCAGATATCC GGGTGGGGA ACCGAAGCAA TCTTGGCGCG ATGTTAATTA

801 ACATAACCTT ATGTATCATA CACATACGAT TTAGGTGACA CTATAGAATA ACATCCACTT TGCCCTTCTC TCCACAGTG TCCACTCCA GGTCCAAC TG
   TGTATTGGAA TACATAGTAT GTGTATGCTA AATCCACTGT GATATCTTAT TGTAGGTGAA ACGGAAGAG AGGTGTCCAC AGGTGAGGT CCAGGTTGAC

901 CACCTCGGTT CTATCGATTG AATTCACCA TGGGATGTC ATGTATCATC CTTTCTTAG TAGCAACTGC AACTGGAGCG TACGCTGAGG TTCAGCTGGT
   GTGGAGCCAA GATAGCTAAC TTAAGGTGGT ACCCTACCAG TACATAGTAG GAAAAGATC ATCGTTGACG TTGACCTCGC ATGCACTCC AAGTCGACCA
   1  M G W S C I I L F L V A T A T G A Y A E V Q L V
      ^start signal peptide      ^start of heavy chain
      ^met                        ^BsiWI

```

**FIG. 34A**



1001 GGAGTCTGGC GGTGGCCCTGG TGCAGCCAGG GGGCTCACTC CGTTTGTCCT GTGCAGCTTC TGGCTTCACC ATTAGTGGTT CTGGATACA CTGGGTGGT  
 CCTCAGACCG CCACCGGACC ACGTCGGTCC CCCGAGTGAG GCAACACAGG CACGTGCAAG ACCGAAGTGG TAATCACCAA GAACCTATGT GACCCACGCA  
 25 E S G G G L V Q P G G S L R L S C A A S G F T I S G S W I H W V R  
 ^CDR-H1  
 1101 CAGGCCCCCG GTAAGGGCCT GGAATGGGTT GCTTGGATTG CTCCTTATAG CGGGCTACT GACTATGCCG ATAGCGTCAA GGGCCGTTTC ACTATAAGCG  
 GTCCGGGGCC CATTCGCCGA CATTCCCGGA CATTACCCAA CGAAGCTAAC GAGGAATATC GCCCGGATGA CTGATACGGC TATCGCAGTT CCGGCAAG TGAATTCGC  
 58 Q A P G K G L E W V A W I A P Y S G A T D Y A D S V K G R F T I S A  
 ^CDR-H2  
 1201 CAGACATC CAAAAACACA GCCTACCTAC AATGAACAG CTTAAGAGCT GAGGACACTG CCGTCTATTA TTGTGCAAGA GAGGGGGCT TGTACTGGGT  
 GTCTGTGTAG GTTTTGTGT CCGATGGATG TTTACTTGTG GAATCTCGA CTCCTGTGAC GGCAGATAAT AACACGTTCT CTCCCCCGA ACATGACCCA  
 92 D T S K N T A Y L Q M N S L R A E D T A V Y Y C A R E G G L Y W V  
 ^CDR-H3  
 1301 GTTCGACTAC TGGGGTCAAG GAACCCCTGGT CACCGTCTCC TCGGCTCCA CCAAGGGCC ATCGGTCTTC CCCCTGGCAC CCTCCTCCAA GAGCACCTCT  
 CAAGCTGATG ACCCCAGTTC CTTGGGACCA GTGGCAGAGG AGCCGAGGT GGTTCGCGG TAGCCAGAAG GGGGACCGTG GGAGGAGGTT CTGCTGGAGA  
 125 F D Y W G Q G T L V T V S S A S T K G P S V F P L A P S S K S T S  
 ^Apal  
 1401 GGGGGCACAG CGGCCCTGGG CTGCCCTGTC AAGGACTACT TCCCGAACC GGTGACGGTG TCGTGGAACT CAGGCGCCCT GACCAGCGGC GTGCACACCT  
 CCCCCGTGTC GCCGGGACCC GACGGACCCAG TTCCTGATGA AGGGCTTGG CCACGTGCCAC AGCACCTGA GTCCGCGGGA CTGGTCGCCG CACGTGTGGA  
 158 G G T A A L G C L V K D Y F P E P V T V S W N S G A L T S G V H T F  
 1501 TCCCCGGCTGT CTTACAGTCC TCAGGACTCT ACTCCCTCAG CAGGTGGTG ACTGTGCCCT CTAGCAGCTT GGGCACCCAG ACCTACATCT GCAACGTGAA  
 AGGGCCGACA GGATTCAGG AGTCCTGAGA TGAGGGAGTC GTCCACCCAC TGACAGGGA GATCGTCGAA CCCGTGGGTC TGGATGTAGA CGTTGCACCT  
 192 P A V L Q S S G L Y S L S S V V T V P S S S L G T Q T Y I C N V N  
 1601 TCACAAGCCC AGCAACACCA AGGTGGACAA GAAAGTTGAG CCAATCTT GTGACAAAAC TCACACATGC CCACCGTGCC CAGCACCTGA ACTCCTGGGG  
 AGTGTTCGGG TCGTGTGGT TCCACCTGTT CTTTCAACTC GGGTTTAGAA CACTGTTTGG AGTGTGTACG GGTGGCAGG GTCTGTGGACT TGAGGACCCC  
 225 H K P S N T K V D K K V E P K S C D K T H T C P P C P A P E L L G

FIG. 34B

1701 GGACCGTCAG TCCTCTCTTT CCCCCCAAAA CCCAAGGACA CCTCATGAT CTCCCGGACC CCTGAGGTCA CATGCGTGGT GGTGGACGTG AGCACAAG  
 CCTGGCAGTC AGAAGGAGAA GGGGGGTTTT GGGTTCTGT GGGAGTACTA GAGGGCTGG GGAATCCAGT GTACGCACCA CCACCTGCAC TCGGTGCTTC  
 258 G P S V F L F P P K P K D T L M I S R T P E V T C V V V D V S H E D  
 1801 ACCCTGAGGT CAAGTTCAAC TGGTACGTGG ACGGCGTGA GGTGCATAAT GCCAAGACAA AGCCGGGGGA GGAGCAGTAC AACAGCACGT ACCGGGTGGT  
 TGGGACTCCA GTTCAAGTTG ACCATGCACC TGCCGCACCT CCACGTATTA CGGTTCTGTT TCGGCGCCCT CCTCGTCATG TTGTCGTGCA TGGCCACCA  
 292 P E V K F N W Y V D G V E V H N A K T K P R E E Q Y N S T Y R V V  
 1901 CAGCGTCTC ACCGTCTCTG ACCAGGACTG GCTGAATGGC AAGGAGTACA AGTCAAGGT CTCCAACAAA GCCCTCCAG CCCCACCGA GAAAACCATC  
 GTCCGAGGAG TGGCAGGAG TGCTCTGAC CGACTTACCG TTCTCTCATGT TCACGTTCCTA GAGGTGTTT CCGGAGGCTC GGGGTAGCT CTTTGTGTAG  
 325 S V L T V L H Q D W L N G K E Y K C K V S N K A L P A P I E K T I  
 2001 TCCAAAGCCA AAGGGCAGC CCGAGAACA CAGTGTACA CCTGCCCCC ATCCCGGGA GAGATGACCA AGAACCAGGT CAGCTGACC TGCTGTGCA  
 AGTTTCTGGT TTCCCGTGG GGCTCTTGGT GTCCACATGT GGGACGGGG TAGGGCCCTT CTCTACTGGT TCTTGTGCA GTGGACTGG ACGGACAGT  
 358 S K A K G Q P R E P Q V Y T L P P S R E E M T K N Q V S L T C L V K  
 2101 AAGGCTCTA TCCAGCGAC ATCGCCGTGG AGTGGGAG CAGTGGGAG CAATGGGAG CCGGAGAACA ACTACAAGAC CACGCCCTCC GTCTGGACT CCGACGGCTC  
 TTCCGAAGAT AGGTGCTG TAGCGGCACC TCACCTCTC GTTACCCGTC GGCTCTTGT TGATGTTCTG GTGCGGAGG CACGACCTGA GGCTGCCGAG  
 392 G F Y P S D I A V E W E S N G Q P E N N Y K T T P P V L D S D G S  
 2201 CTCTCTCTC TACAGCAAGC TCACCGTGA CAAGAGCAGG TGGCAGCAG GGAAGTCTT CTCATGCTCC GTGATGCAAG AGGCTCTGCA CAACCACTAC  
 GAAGAAGGAG ATGTCGTTG AGTGGCACCT GTTCTCGTCC ACCGTCGTC CCTTGCAGAA GAGTACGAGG CACTACGTAC TCCGAGACGT GTTGTGATG  
 425 F F L Y S K L T V D K S R W Q Q G N V F S C S V M H E A L H N H Y  
 2301 ACGCAGAGA GCCTCTCCCT GTCTCCGGGT AAATGAGTGC GACGGCCCTA GATCGACCT GCAGAAGCTT GGCGGCCATG GCCCAACTTG TTTATTGCA  
 TGCGTCTCT CGGAGAGGA CAGAGGCCCA TTTACTCAG CTGCGGGGAT CTCAGCTGGA CGTCTTCGAA CCGCGGGTAC CGGGTTGAAC AAATAACGTC  
 458 T Q K S L S L S P G K O  
 2401 CTTATAATGG TTACAATAA AGCAATAGCA TCACAAATTT CACAAATAA GCATTTTTT CACTGCATC TAGTTGTGGT TTGTCCAAAC TCATCAATGT  
 GAATATTACC AATGTTTAT TCGTTATCGT AGTGTATAA GTGTTTATTT CGTAAAAA GTGACGTAAG ATCAACACCA AACAGGTTG AGTAGTTACA

FIG. 34c

2501 ATCTTATCAT GTCTGGATCG ATCGGGGAATT AATTCGGCGC AGCACCATGG CCTGAATAAA CCTCTGAAG AGGAACATTGG TTAGGTACCT TCTGAGGCGG  
 TAGAATAGTA CAGACCTAGC TAGCCCTTAA TTAAGCCGCG TCGTGGTACC GGACTTTATT GGAGACTTTC TCCTTGAACC AATCCATGGA AGACTCCGCG  
 2601 AAAGAACCAT CTGTGGGAATG TGTGTAGTT AGGGTGTGGA AAGTCCCCAG GCTCCCCCAG AGGCAGAGT ATGCAAAAGCA TGCATCTCAA TTAGTCAGCA  
 TTTCTTGGTA GACACCTTAC ACACAGTCAA TCCACACCTT TTAGGGGCTC CGAGGGTCTG TCCGTCTTCA TACGTTTCTT ACGTAGAGTT AATCAGTCGT  
 2701 ACCAGGTGTG GAAAGTCCCC AGGCTCCCCA GCAGGCAGAA GTATGCAAG CATGCATCTC AATTAGTCAG CAACCAATAGT CCGGCCCTTA ACTCCGCCCCA  
 TGGTCCACAC CTTTCAGGGG TCCGAGGGGT CGTCCGTCTT CATACGTTTC GTACGTAGAG TTAATCAGTC GTTGTATCA GGGCGGGGAT TGAGCGGGGT  
 2801 TCCCGCCCCCT AACTCCGCCC AGTTCCGCCC ATCTCCGCC CCATGGCTGA CTAATTTTTT TTATTTATGC AGAGGCGGAG GCCGCCCTGG CCTCTGAGCT  
 AGGGCGGGGA TTGAGGCGGG TCAAGGCGGG TAAGAGGCGG GGTACCGACT GATTAATAAA AATAAATACG TCTCCGGCTC CCGCGGAGCC GGAGACTCGA  
 2901 ATTCCAGAAG TAGTGAGGAG GCTTTTGTGG AGGCCTAGGC TTTTGCAAA AGCTGTAAAC AGCTTGGCAC TGGCGTCTGT TTTACAACGT CGTGACTGGG  
 TAAGGTCTTC ATCACTCCTC CGAAAAAAC TCCGGATCCG AAAACGTTTT TCGACAATG TCGAACCGTG ACCGGCAGCA AATGTGTGA GCACGTGACC  
 3001 AAAACCCCTGG CGTTACCCAA CTTAATCGCC TTGCAGCACA TCCCCCCTTC GCCAGTTGG GTAAATAGCGA AGAGGCCCGC ACCGATCGCC CTTCCCAACA  
 TTTTGGGACC GCAATGGGTT GAATTAGCGG AAGTCTGTGT AGGGGGAAG CGGTCAACCG CATTTATCGCT TCTCCGGGCG TGGCTAGCGG GAAGGTTGT  
 3101 GTTGGGTAGC CTGAATGGCG AATGGCGCCT GATGCGGTAT TTTCTCTCTTA CGCATCTGTG CCGTATTTCA CACCGCATAC GTCAAAGCAA CCATAGTACG  
 CAACGCATCG GACTTACCGC TTACCGCGGA CTACGCCATA AAAGAGGAAT GCGTAGACAC GCCATAAAGT GTGGCGTATG CAGTTTCTGT GTATCATGTC  
 3201 CGCCCTGTAG CGGCGCATTA AGCGGGCGG GTGTGGTGGT TACGCGCAGC GTGACCGCTA CACTTGGCAG CGCCCTAGCG CCGCTCTCTT TCGCTTCTTT  
 GCGGGACATC GCCGCGTAAT TCGCGCCGCC CACACCACA ATGCGGTCTG CACTGGCGAT GTGAACGGTC GCGGATCGC GGGCGAGGAA AGCGAAAGAA  
 3301 CCTTCTCTTT CTGCGCACGT TCGCCGGGCTT TCCCGGTCAA GCTCTAAATC GGGGCTCCC TTTAGGGTTC CGATTAGTG CTTTACGGCA CCTCGACCCC  
 GGAAGGAAA GACCGGTGCA AGCGGCCGAA AGGGGCAGTT CGAGATTAG CCCCCGAGG AATCCCAAAG GCTAATCAC GAAATGCCGT GGAGCTGGGG  
 3401 AAAAAACTTG ATTTGGGTGA TGGTTACGT AGTGGGCCAT CGCCCTGATA GACGGTTTTT CGCCCTTTGA CGTTGGAGTC CACGTTCTTT AATAGTGGAC  
 TTTTGTGAAC TAAACCCACT ACCAATGCA TCACCCGGTA CCGGGACTAT CTGCCAAAAA GGGGGAACCT GCACTCAG GTGCAAGAAA TTATCACCTG

FIG. 34 D

3501 TCTTGTTCAC AACTGGAACA ACACTCAACC CTATCTCGGG CTATTCTTTT GATTATTAAG GGATTTTGCC GATTTCCGCC TATTGGTTAA AAAATGAGCT  
 AGAACAAAGGT TTGACCTTGT TGTGAGTTGG GATAGAGCCC GATAAGAAA CTAATAATTC CTAAGCCGG CTAAGCCGG ATAACCAATT TTTTACTCGA  
  
 3601 GATTTAACAA AAATTTAACG CGAATTTTAA CAAAATATTA AGTTTACAA TTTTATGTTG CACTCTCAGT ACAATCTGCT CTGATGCCGC ATAGTTAAGC  
 CTAATAATGTT TTTAAATTCG GCTTAAATTT GTTTTATAAT TGCATAATGTT AAAATACCAC GTGAGAGTCA TGTTAGACGA GACTACGGCG TATCAATTCG  
  
 3701 CAACTCCGCT ATCGCTACGT GACTGGGTCA TGGCTGGCC CCGACACCCG CCAACACCCG CTGACGGGCT TGTCTGCTCC CGGCATCCGC  
 GTTGAGCGCA TAGCGATGCA CTGACCCAGT ACCGACGGCG GGTGTGGGC GGTGTGGGC GACTGCCCG GACTGCCCG ACAGACGAGG GCCGTAGGCG  
  
 3801 TTACAGACAA GCTGTGACCG TCTCCGGGAG CTGCATGTGT CAGAGGTTT CACCGTCATC ACCGAAACGC GCGAGGCGT ATTCTTGAAG ACGAAAGGC  
 AATGCTCTGTT CGACACTGGC AGAGGCCCTC GACGTACACA GTCTCCAAA GTGGCAGTAG TGGCTTTGCG CGCTCCGTCA TAAGAACTTC TGCTTTCCCG  
  
 3901 CTCGTGATAC GCTATTTTT ATAGGTTAAT GTCATGATAA TAATGGTTTC TTAGACGTCA GTGGCAGT TTCCGGGAAA TGTGCGCGGA ACCCCTATTT  
 GAGCACTATG CGGATAAAAA TATCCAATTA CAGTACTATT ATTACCAAG AATCTGCAGT CCACCGTGAA AAGCCCTTT ACACGCCCT TGGGGATAAA  
  
 4001 GTTTATTTTT CTAATATCAT TCAATATGT ATCCGCTCAT GAGACAATAA CCTTGATAA TGCTTCAATA ATATTGAAA AGGAAGAGTA TGAGTATTC  
 CAAATAAAAA GATTTATGTA AGTTATACA TAGGCGAGTA CTCTGTTATT GGGACTATTT ACGAAGTTAT TATAACTTTT TCCTTCTCAT ACTCATAGT  
  
 4101 ACATTTCCGT GTCGCCCCTA TTCCCTTTTT TCGGGCATTT TGCCCTTCTG TTTTGTCTCA CCCAGAAAAG CTGGTGAAAG TAAAAGATGC TGAAGATCAG  
 TGTAAAGGCA CAGCGGGAAT AAGGAAAAA ACGCGTAAA ACGGAAGGAC AAAAACGAGT GGGTCTTTGC GACCACCTTC ATTTTCTAGC ACTTCTAGTC  
  
 4201 TTGGGTGCAC GAGTGGGTTA CATCGAACTG GATCTCAACA GCGGTAAGAT CCTTGAGAGT TTTCGCCCGG AAGAACGTTT TCCAATGATG AGCACITTTA  
 AACCACGCTG CTCACCCCAAT GTAGCTTGAC CTAGAGTTGT CGCCATTCTA GGAACCTCTCA AAAGCGGGGC TTCTTGCAAA AGGTACTAC TCGTGAATAAT  
  
 4301 AAGTCTGCT ATGTGGCGCG GTATTATCCC GTGATGACGC CCGGCAAGAG CAACTCGGTC GCGCATACA CTATTCTCAG AATGACTTGG TTGAGTACTC  
 TTCAAGACGA TACACCGCGC CATAATAGG CACTACTGCG GCCCGTTCTC GTTGAGCCAG CGGCTATGT GATAAGATC TTACTGAACC AACTCATGAG  
  
 1401 ACCAGTCACA GAAAAGCATC TTACGGATGG CATGACAGTA AGAGAATTAT GCAGTGCTGC CATAACCATG AGTGATAACA CTGCGGCGCA CTTACTTCTG  
 TGGTCAGTGT CTTTTCGTAG AATGCCTACC GTACTGTGAT TCTCTTAATA CGTACGAGC GTATTGGTAC TCACTATTGT GACGCGGTT GAATGAAGAC  
  
 1501 ACAACGATCG GAGGACCGAA GGAGCTAAC GCTTTTTTTC ACAACATGGG GGATCATGTA ACTCGCCTTG ATCGTTGGA ACCGAGCTG AATGAAGCA  
 TGTGTGCTAG CTCCTGGCTT CCTCGATGG CGAAAAACG TGTGTATACC CCTAGTACAT TGAGCGGAAC TAGCAACCT TGCCCTCGAC TTACTTCTGCT

FIG. 34E

4601 TACCAAAACGA CGAGCGTGAC ACCACGATGC CAGCAGCAAT GGCAACAACG TTGCGCAAAAC TATTAACCTGG CGAACTACTT ACTCTAGCTT CCCGGCAACA  
 ATGGTTTGCT GCTCGCACTG TGGTGCTAGC GTGCTCGTTA CCGTTGTGC AACCGTTTG ATAATTGACC GCTTGATGAA TGAGATCGAA GGGCCGTTGT  
 4701 ATTAATAGAC TGGATGAGG CGGATAAAGT TGCAGGACCA CTCTGCGCT CGGCCCTTCC GGCTGGCTGG TTTATTGCTG ATAAATCTGG AGCGGGTGAG  
 TAATTATCTG ACCTACCTCC GCCTATTTCA AGTCTCTGGT GAAGACCGGA GCCGGGAAGG CCGACCGAGC AAATAACGAC TATTIAGACC TCGGCCACTC  
 4801 CGTGGGTCTC GGGTATCAT TGCAGCACTG GGGCCAGATG GTAAGCCCTC CCGATTCGTA GTTATCTACA CGACGGGAG TCAGGCAACT ATGGATGAAC  
 GCACCCAGAG CGCCATAGTA ACGTCGTGAC CCGGTCTAC CATTCGGGAG GGCATAGCAT CAATAGATGT GCTGCCCTC AGTCCGTTGA TACCTACTTG  
 4901 GAAATAGACA GATCGCTGAG ATAGGTGCCT CACTGATTAA GCATTGGTAA CTGTCAGACC AAGTTACTC ATATATACTT TAGATTGATT TAAAACTTCA  
 CTTTATCTGT CTAGCGACTC TATCCACGGA GTGACTTAAT CGTAACTATT GACAGTCTGG TTCAAATGAG TATATATGAA ATCTAACTAA ATTTTGAAGT  
 5001 TTTTAAATTT AAAAGGATCT AGGTGAAGAT CCTTTTGTAT AATCTCATGA CCAAAATCCC TTAACGTGAG TTTTCGTGCC ACTGAGCGTC AGACCCCGTA  
 AAAAAATAA TTTTCTCTAG TCCACTCTTA GGAAAACTA TTAGAGTACT GGTTTTAGG AATTGCACCT AAAAGCAAGG TGACTCCGAG TCTGGGGCAT  
 5101 GAAAAGATCA AAGGATCTTC TTGATATCCT TTTTCTCTGC GCGTAATCTG CTGCTTGCAA AAAAAAAC CACCGCTACC AGCGGTGGTT TGTTTGCCGG  
 CTTTCTTAGT TTCTTAGAAG AACTCTAGGA AAAAAAGAG CGCATTAGAC GACGAACGTT TGTTTTGTG GTGGCGATGG TCGCCACCAA ACAAAACGGCC  
 5201 ATCAAGAGCT ACCAATCTT TTTCCGAAG TAACTGGCTT CAGCAGAGCG CAGATACCAA ATACTGTCTT TCTAGTGATG CCGTAGTTAG GCCACCACTT  
 TAGTTCTCGA TGGTTGAGAA AAAGGCTTCC ATTGACCGAA GTGCTCTCGC GTCTATGGTT TATGACAGGA AGATCACATC GGCATCAATC CCGTGGTGAA  
 5301 CAAGAAGTCT GTAGCACCGC CTACATACCT CGCTCTGCTA ATCTGTATC CAGTGGCTGC TGCCAGTGGC GATAAGTGT GTCTTACCGG GTTGGACTCA  
 GTTCTTGAGA CATCGTGGCG GATGTATGGA GCGAGACGAT TAGGACAATG GTCACCGAGC ACGTCAACCG CTATTACGCA CAGAATGGCC CAACCTGAGT  
 5401 AGACGATAGT TACCGGATAA GGGCAGCGG TCGGGCTGAA CCGGGGGTTC GTGCACACAG CCGAGCTTGG AGCGAACGAC CTACACCGAA CTGAGATACC  
 TCTGCTATCA ATGGCCTATT CCGGTCGCC AGCCCGACTT GCCCCCCAAG CAGGTGTGTC GGGTCGAACC TCGTGTGCTG GATGTGGCTT GACTCTATGG  
 5501 TACACCGTGA GCATTGAGAA AGCGCCACGC TTCCCGAAGG GAGAAAGGG GACAGGTATC CCGTAAGCGG CAGGGTCGGA ACAGGAGAGC GCACGAGGGA  
 ATGTGCACT CGTAATCTT TCGCGGTGCG AAGGGCTTCC CTCTTTCGC CTGTCCATAG GCCATTGCC GTCCAGCCT TGTCTCTCTCG CGTGTCTCTT  
 601 GCTTCCAGG GGAACGGCT GGTATCTTTA TAGTCTGTG GGTTCGCTC ACCCTGACT TGAGCGTCTA TTTTGTGTAT GCTCGTCAGG GGGCGGAGC  
 CGAAGGTCCC CCTTTCGGA CCATAGAAAT ATCAGGACAG CCGAAAGCGG TGGAGACTGA ACTCGCAGCT AAAAACACTA CGAGCAGTCC CCCCCCTCTC

FIG. 34 F

5701 CTATGGGAAA ACGCCAGCAA CGCGGCCCTTT TTACCGTTCC TGGCCCTTTG CTGGCCCTTT GCTCACATGT TCTTTCCTGC GTTATCCCCT GATTCTGTGG  
GATACCTTTT TCGCGTCGTT GCGCCGAAA AATGCCAAGG ACCGGAAAAC GACCGGAAA CGAGTGACA AGAAGGACG CAATAGGGA CTAAGACACC

5801 ATAAACGTAT TACCGCCCTTT GAGTGAGTG ATACCGCTCG CCGCAGCCGA ACGACCGAGC GCAGCGAGTC AGTGAGCGAG GAAGCGGAAG AGCGCCCAAT  
TATTGGCATA ATGGCGGAAA CTCACTCGAC TATGGCGAGC GCGCTGGCT TGCTGGCTCG CGTCGCTCAG TCACTCGCTC CTTCGCCCTC TCGCGGGTTA

5901 ACGCAAACCG CCTCTCCCG CGCGTTGGCC GATTCATTAA TCCAACTGGC ACGACAGGTT TCCCGACTGG AAAGCGGGCA GTGAGCGCAA CGCAATTAAT  
TGCGTTTGGC GGAGAGGGGC GCGCAACCG CTAAGTAATT AGGTTGACCG TGCTGTCCAA AGGCTGACC TTTCGCCCGT CACTCGCGTT GCGTTAATTA

6001 GTGAGTTACC TCACTCATTG GGCACCCAG GCTTTACACT TTATGCTTCC GGCTCGTATG TTGTGTGGAA TTGTGAGCGG ATAACAATTT CACACAGGAA  
CACTCAATGG AGTGAGTAAT CCGTGGGCTC CGAAATGTGA AATACGAAG CCGAGCATAC AACACACCTT AACACTGCC TATTGTTAAA GTGTGTCTTT

6101 ACAGCTATGA CCATGATTAC GAATTA  
TGTCGATACT GGTACTAATG CTTAAT

FIG. 34

## LC Frequency

28	S	N	V	D	G	I	T	L	X	
511	511	262	258	186	178	44	39	16	35	
29	I	S	V	G	N	X				
612	612	272	254	192	147	70				
30	S	N	K	G	R	Y	T	D	A	X
849	849	176	169	86	81	63	29	28	17	45
31	S	N	T	R	I	D	K	G	X	
676	676	496	170	47	29	28	25	18	53	
32	Y	N	W	F	S	D	R	X		
1055	1055	128	97	77	61	40	25	69		
50	G	A	D	W	K	L	E	S	X	
386	386	341	294	151	116	91	39	30	82	
53	S	N	T	K	I	R	X			
545	545	438	407	41	23	23	58			
91	Y	S	R	A	G	H	X			
849	849	196	169	118	61	41	148			
92	Y	G	N	S	D	L	T	H	I	X
362	362	356	248	193	114	94	64	43	38	91
93	S	N	Q	T	H	G	D	R	X	
738	738	346	117	101	66	51	47	35	112	
94	S	T	W	Y	L	F	A	P	V	I
386	386	365	288	172	114	79	46	43	33	24
96	L	Y	W	F	I	R	P	X	N	X
264	264	205	176	140	117	115	46	121	18	40

FIG. 35

Residue	Natural Diversity	Diversity < DNA codon	% good	% covering
L1-28	SNVDGI	SNVDGI<RDT>	100%	94%
L1-29	ISVGN	ISVG<RKT>	100%	86%
L1-29		IV<RTT>	100%	56%
L1-30	SNKGRYTDA	SNKGGRTTDAAE<RVW>	92%	93%
L1-31	SNTRIDKG	SNTRDKGGAAE<RVW>	75%	95%
L1-31		SNTTRIIE<ANW>	100%	94%
L1-32	YNWFSDR	YNFSDATIV<DHT>	55%	88%
L1-32		YFS<THT>	100%	77%
L2-50	GADWKLES	GAWLSV<KBG>	83%	67%
L2-53	SNTKIR	SNT<AVC>	100%	90%
L3-91	YSRAGH	YSAD<KMT>	75%	74%
		YS<TMT>	100%	66%
L3-92	YGNSDLTHI	YNSDTIFAV<DHT>	67%	64%
		YNSDTA<DMC>	83%	62%
L3-93	SNQTHGDR	SNTGDA<RVT>	83%	80%
		SNTDYAFIV<DHT>	44%	76%
L3-94	STWYLFAPVI	STYLFAPVINDH<NHT>	75%	78%
		STYFIN<WHT>	83%	43%
L3-96	LYWFIRP	LYFPHS<YHT>	67%	52%
		LYFIHN<HWT>	67%	58%
		LFI<HTT>	100%	42%
		LLWR<YKG>	100%	47%
		YF<TWT>	100%	29%

**FIG.** 36



**Light Chain Designed Diversity**  
Diversity:  $\sim 2.9 \times 10^9$

**CDR-L1: diversity  $\sim 7 \times 10^3$**

28	29	30	31	32
RDT	RTT	RVW	RVW	DHT
D	I	D	D	A
G	V	E	E	D
I		G	G	F
N		K	K	I
S		N	N	N
V		S	S	S
		T	T	T
		R	R	V
				Y

**CDR-L2: diversity = 18**

50	53
KBG	AVC
A	N
G	S
L	T
S	
V	
W	

**CDR-L3: diversity  $\sim 2.3 \times 10^4$**

91	92	93	94	96
KMT	DHT	DHT	NHT	YHT
A	A	A	A	F
D	D	D	D	H
S	F	F	F	L
Y	I	I	H	P
	N	N	I	S
	S	S	L	Y
	T	T	N	
	V	V	P	
	Y	Y	S	
			T	
			V	
			V	
			Y	

**FIG. 37**

**Light Chain Designed Diversity**  
Diversity:  $\sim 6.1 \times 10^8$

**CDR-L1: diversity  $\sim 3.4 \times 10^3$**

28	29	30	31	32
RDT	RTT	RVW	ANW	THT
D	I	D	I	F
G	V	E	K	S
I		G	N	Y
N		K	R	
S		N	S	
V		S	T	
		T		
		V		

**CDR-L2: diversity = 18**

50	53
KBG	AVC
A	N
G	S
L	T
S	
V	
W	

**CDR-L3: diversity  $\sim 1.0 \times 10^4$**

91	92	93	94	96
KMT	DMC	RVT	NHT	YHT
A	A	A	A	F
D	D	D	D	H
S	N	G	F	L
Y	S	N	H	P
	T	S	I	S
	Y	T	L	Y
			N	
			P	
			S	
			T	
			V	
			Y	

**FIG. 38**

**Light Chain Designed Diversity****CDR-L3: diversity  $\sim 1.3 \times 10^3$** 

91	92	93	94	96
TMT	DMC	RVT	WHT	HTT
S	A	A	F	F
Y	D	D	I	I
	N	G	N	L
	S	N	S	
	T	S	T	
	Y	T	Y	

**FIG. 39****CDR-L1**

28	29	30	31	32
RDT	RTT	RVW	RVW	DHT
D	I	D	D	A
G	V	E	E	D
I		G	G	F
N		K	K	I
S		N	N	N
V		S	S	S
		T	T	T
		V	V	V
				Y

**CDR-L2**

50	53
DVK	AVM
A	N
G	K
L	R
S	S
V	T2
W	

**CDR-L3**

91	92	93	94	96
NRT	NRT	RVM	NNK	TDK
C	C	A2	A	C
D	D	D	C	F
G	G	E	D	L
H	H	G2	E	W
N	N	K	F	Y
R	R	N	G	*
S	S	R	H	
Y	Y	S	I	
		T2	L	
			M	
			N	
			P	
			Q	
			R	
			etc	
			*	

\*Amber stop codon is encoded by the degenerate codon

**FIG. 40**

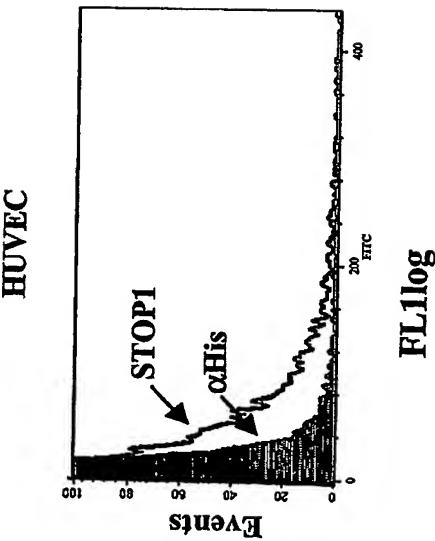
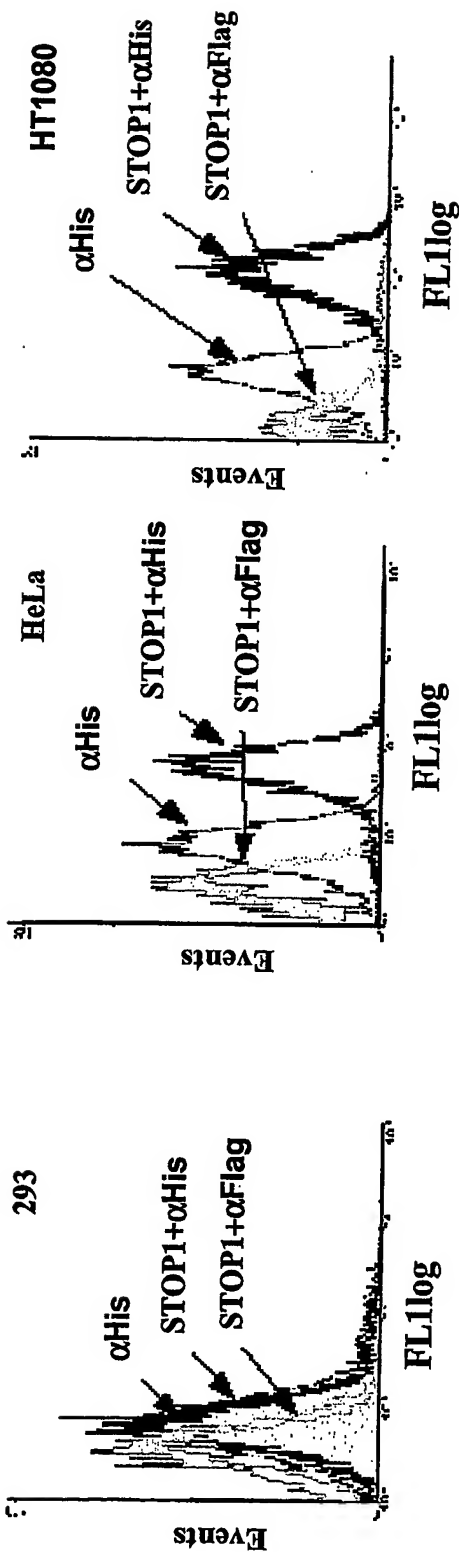
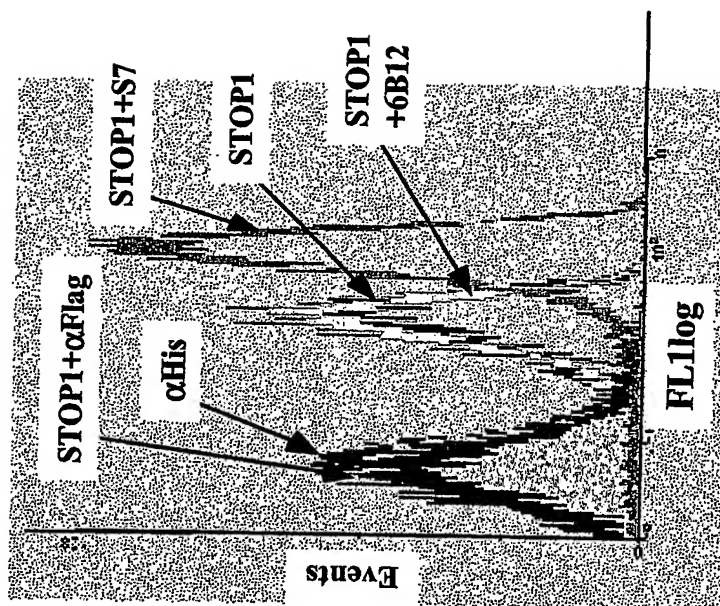
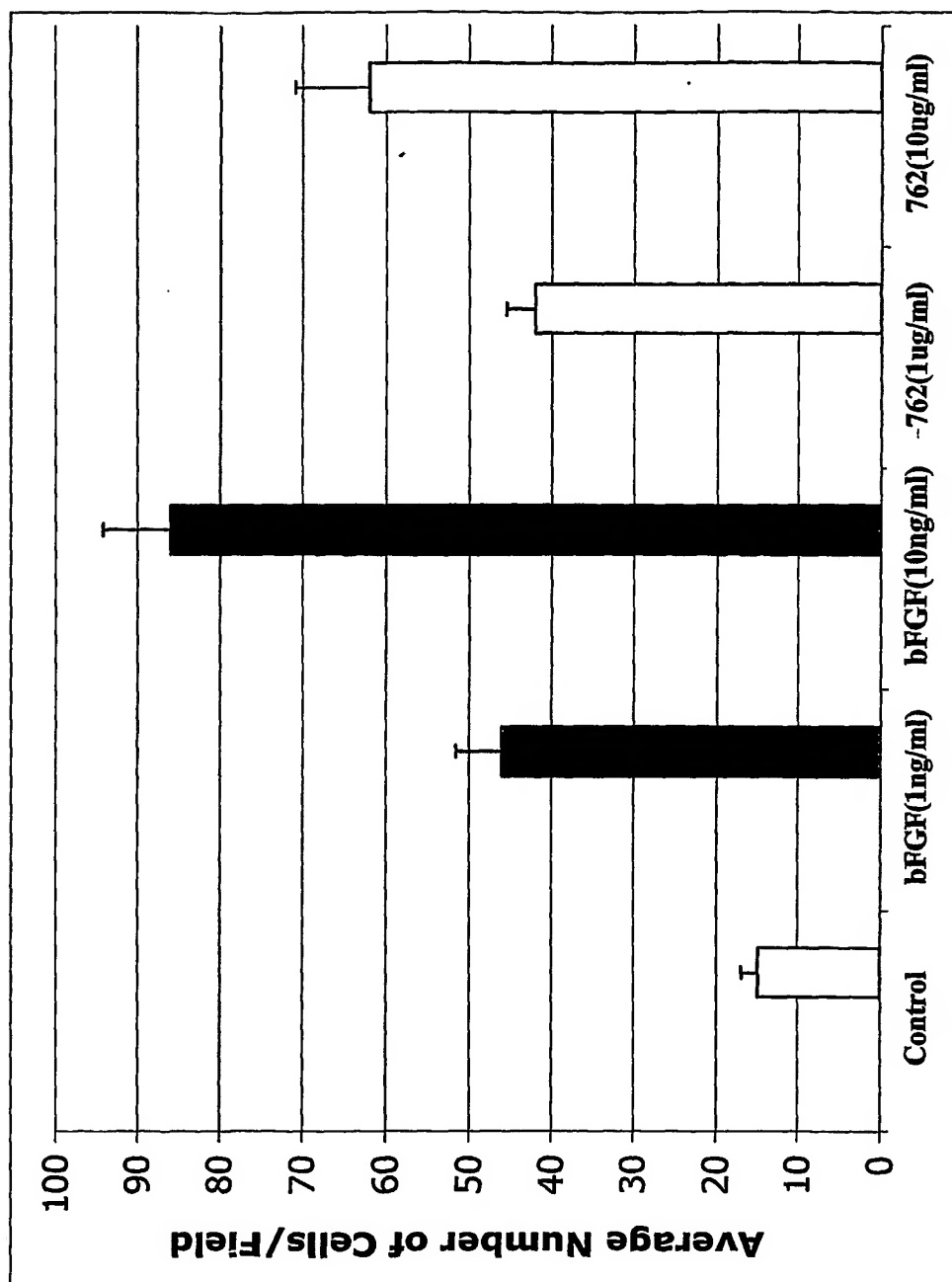
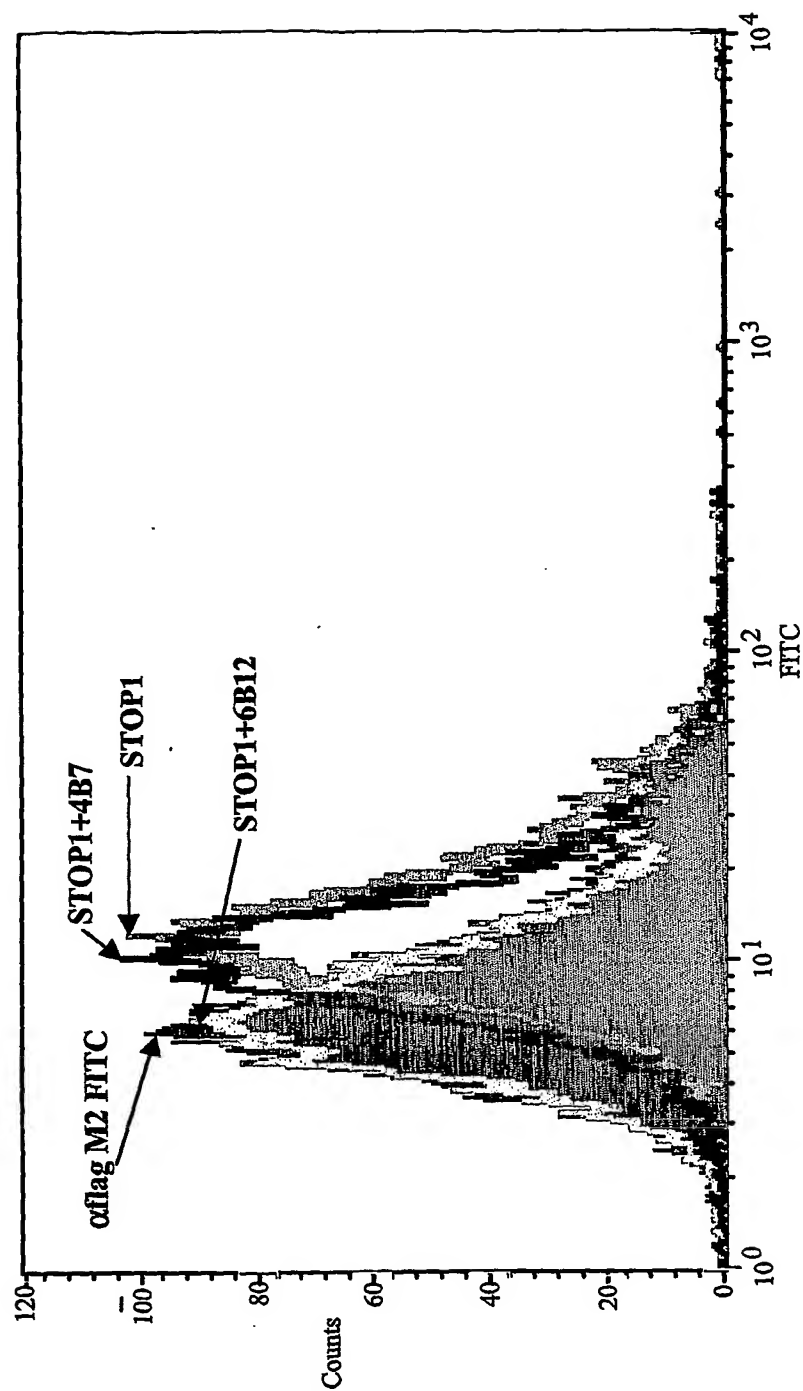


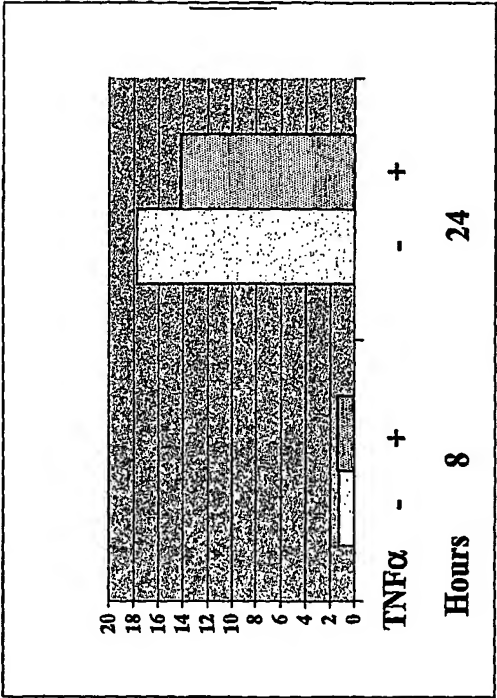
FIG.41

**FIG.42**

**FIG.43**

**FIG.44**

A.



B.

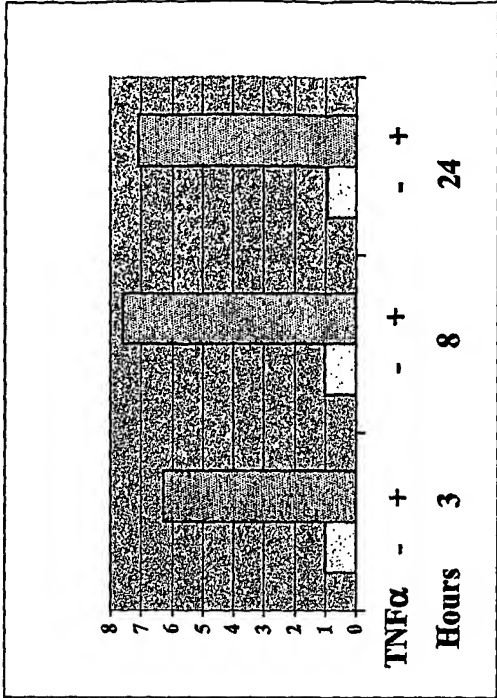


FIG.45

This Page is inserted by IFW Indexing and Scanning  
Operations and is not part of the Official Record

## BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☒ BLACK BORDERS
- ☒ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
- ☒ FADED TEXT OR DRAWING
- ☒ BLURED OR ILLEGIBLE TEXT OR DRAWING
- ☒ SKEWED/SLANTED IMAGES
- ☐ COLORED OR BLACK AND WHITE PHOTOGRAPHS
- ☐ GRAY SCALE DOCUMENTS
- ☐ LINES OR MARKS ON ORIGINAL DOCUMENT
- ☐ REPERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
- ☐ OTHER: \_\_\_\_\_

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning documents *will not* correct images  
problems checked, please do not report the  
problems to the IFW Image Problem Mailbox**